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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 07:30:51 ; Search time 701.41 Seconds
(without alignments)
11157.588 Million cell updates/sec

Title: US-10-051-307-1

Perfect score: 1595

Sequence: 1 gtaatacagactactatagg.....tggtaggtgtgtgttttc 1595

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1595	100.0	1595	14 US-10-051-307-1	Sequence 1, Appli
2	1482.2	92.9	1598	14 US-10-051-307-2	Sequence 2, Appli
3	1362.4	85.4	1546	14 US-10-051-307-3	Sequence 3, Appli
C 4	293.4	18.4	510	16 US-10-341-961A-371	Sequence 371, App
C 5	195.6	12.3	735	9 US-09-938-842A-2118	Sequence 2118, Ap
C 6	195.6	12.3	735	11 US-09-938-842A-2118	Sequence 2118, Ap
C 7	195.6	12.3	950	9 US-09-770-445-334	Sequence 334, App
C 8	173	10.8	1956	13 US-10-424-599-36321	Sequence 36321, A
C 9	170.4	10.7	875	12 US-10-636-396-4	Sequence 4, Appli
C 10	170.4	10.7	875	17 US-10-636-026-4	Sequence 4, Appli
C 11	167	10.5	909	13 US-10-424-599-103619	Sequence 103619,
C 12	137.4	8.6	717	15 US-10-259-165-389	Sequence 389, App
C 13	137.4	8.6	720	15 US-10-259-165-41	Sequence 41, Appl
C 14	135.2	8.5	1006	17 US-10-437-963-86607	Sequence 86607, A

C 15	132	8.3	1173	13 US-10-424-599-7736	Sequence 7736, Ap
C 16	126.6	7.9	901	13 US-10-424-599-7737	Sequence 7737, Ap
C 17	124.2	7.8	696	15 US-10-259-165-353	Sequence 353, App
C 18	124.2	7.8	699	15 US-10-259-165-109	Sequence 109, App
C 19	124.2	7.8	1052	17 US-10-437-963-89569	Sequence 89569, A
C 20	122.2	7.7	1020	15 US-10-259-165-571	Sequence 571, App
C 21	122.2	7.7	1020	16 US-10-260-238-3136	Sequence 3136, Ap
C 22	120.4	7.5	879	16 US-10-260-238-49	Sequence 49, Appl
C 23	120.2	7.5	922	16 US-10-260-238-4067	Sequence 4067, Ap
C 24	118.8	7.4	805	16 US-10-260-238-4061	Sequence 4061, Ap
C 25	116.8	7.3	911	13 US-10-435-114-27634	Sequence 27634, A
C 26	106.8	6.7	343	9 US-09-770-791-806	Sequence 806, App
C 27	106.2	6.7	808	9 US-09-966-881-46	Sequence 46, Appl
C 28	103.2	6.5	633	15 US-10-259-165-532	Sequence 532, App
C 29	103.2	6.5	633	16 US-10-437-963-59877	Sequence 59877, A
C 30	97.6	6.1	1950	17 US-10-437-963-16245	Sequence 16245, A
C 31	94.2	5.9	3630	17 US-10-437-963-16245	Sequence 1, Appli
C 32	90.6	5.7	621	15 US-10-175-389-9	Sequence 9, Appli
C 33	89	5.6	621	15 US-10-175-389-9	Sequence 15621, A
C 34	88.8	5.6	869	17 US-10-437-963-15621	Sequence 24457, A
C 35	87.2	5.5	1528	13 US-10-425-114-24457	Sequence 3135, Ap
C 36	84.8	5.3	728	16 US-10-260-238-3135	Sequence 82389, A
C 37	81.4	5.1	730	13 US-10-425-114-25389	Sequence 82389, A
C 38	77.2	4.8	935	17 US-10-437-963-82256	Sequence 229, App
C 39	76.4	4.8	777	15 US-10-259-165-329	Sequence 630, App
C 40	75.8	4.8	695	15 US-10-259-165-330	Sequence 23076, A
C 41	75	4.7	826	13 US-10-425-114-23076	Sequence 16928, A
C 42	74.8	4.7	973	17 US-10-437-963-16928	Sequence 1, Appli
C 43	71	4.5	3673778	15 US-10-312-841-1	Sequence 6, Appli
C 44	70.4	4.4	529	14 US-10-051-307-6	Sequence 1, Appli
C 45	69.6	4.4	3673778	15 US-10-312-841-1	

ALIGNMENTS

RESULT 1

US-10-051-307-1
; Sequence 1, Application US/10051307
; Publication No. US20020170095A1
; GENERAL INFORMATION:
; APPLICANT: SHI, ZIYU
; APPLICANT: SHI, LIFANG
; APPLICANT: HOOKER, BRIAN S.
; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
; FILE REFERENCE: 059440/0141
; CURRENT APPLICATION NUMBER: US/10/051,307
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,224
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-051-307-1

Query Match	100.0%	Score 1595;	DB 14;	Length 1595;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1595;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GTAATACGACTACTATAGGCAACGCGGTGTCAGCGCCCTGGTGTATCTTTGTTCA	60	
Db	1	GTAATACGACTACTATAGGCAACGCGGTGTCAGCGCCCTGGTGTATCTTTGTTCA	60	
Qy	61	AAAAATGAAAGACGCTAGGACCATGGCTGGTGCAACAATATCTTGCCTC	120	
Db	61	AAAAATGAAAGACGCTAGGACCATGGCTGGTGCAACAATATCTTGCCTC	120	
Qy	121	CAAAATGCTACAGGATTTACATCTCCCGGTACTTTAAAGTTGACCAAGGCGCATTCAC	180	
Db	121	CAAAATGCTACAGGATTTACATCTCCCGGTACTTTAAAGTTGACCAAGGCGCATTCAC	180	

Applicant

Qy 181 CATTTATATTTGGCGTGCATTTGAATTTGGGCAATTTCCCTCCACTTTGGATTAGTCGGGG 240
 Db 181 CATTTATATTTGGCGTGCATTTGAATTTGGGCAATTTCCCTCCACTTTGGATTAGTCGGGG 240
 Qy 241 CGAAGTCATCGGTATATTAATTAATCCATCACTAAAGAAATGTCGCAAAATCTAAGTTGT 300
 Db 241 CGAAGTCATCGGTATATTAATTAATCCATCACTAAAGAAATGTCGCAAAATCTAAGTTGT 300
 Qy 301 TGAAGTCATCGGTATATTAATTAATCCATCACTAAAGAAATGTCGCAAAATCTAAGTTGT 360
 Db 301 TGAAGTCATCGGTATATTAATTAATCCATCACTAAAGAAATGTCGCAAAATCTAAGTTGT 360
 Qy 361 GCAGGACACCAACCAATCACTAGTCATGCAAGAAATCTTACGAGCAACCATCGAAGTTAC 420
 Db 361 GCAGGACACCAACCAATCACTAGTCATGCAAGAAATCTTACGAGCAACCATCGAAGTTAC 420
 Qy 421 ATCCAGTACGACCCCATATATCTGCTAGTCCATCTAGTGGCCCTTAGCGGCATCAATGACCCACA 480
 Db 421 ATCCAGTACGACCCCATATATCTGCTAGTCCATCTAGTGGCCCTTAGCGGCATCAATGACCCACA 480
 Qy 481 TTTGGCCCCGATCGAAGCGTGGGCAACCGCTTTGGGGTGCATGCGGCCCAACGATGTA 540
 Db 481 TTTGGCCCCGATCGAAGCGTGGGCAACCGCTTTGGGGTGCATGCGGCCCAACGATGTA 540
 Qy 541 TGGACGTTCTGCGTACCTCGATAGTGGGAGCATAGTGAAGTCACAAAGCAAGAG 600
 Db 541 TGGACGTTCTGCGTACCTCGATAGTGGGAGCATAGTGAAGTCACAAAGCAAGAG 600
 Qy 601 GGGAAGCAACCAAGCAATCTCAAGTACGCCATCTTTGTTGAAATTTATATGTTGGACAAA 660
 Db 601 GGGAAGCAACCAAGCAATCTCAAGTACGCCATCTTTGTTGAAATTTATATGTTGGACAAA 660
 Qy 661 TTATTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCACTACGATATTAATCG 720
 Db 661 TTATTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCACTACGATATTAATCG 720
 Qy 721 TATATATAGCAATATCATATCTTGTACTATTAATAAGCAATATATTAATCAATATGATTT 780
 Db 721 TATATATAGCAATATCATATCTTGTACTATTAATAAGCAATATATTAATCAATATGATTT 780
 Qy 781 GGTAAAGCTTGAGTGGAAATATGTAAGAGCGGCTTAATAATTAATTAATTTATGAAAT 840
 Db 781 GGTAAAGCTTGAGTGGAAATATGTAAGAGCGGCTTAATAATTAATTAATTTATGAAAT 840
 Qy 841 ATAGCCTATAGTACAAAGTTAACTTTATTTGGTGATACTTTGACATATAAATCTCTGTA 900
 Db 841 ATAGCCTATAGTACAAAGTTAACTTTATTTGGTGATACTTTGACATATAAATCTCTGTA 900
 Qy 901 CGTGACGGAATTTTCTTAAACATAAATATTAATAAGCAAGCTATTTTCAGATTTTCGTG 960
 Db 901 CGTGACGGAATTTTCTTAAACATAAATATTAATAAGCAAGCTATTTTCAGATTTTCGTG 960
 Qy 961 GCCAAGTTTCTGCACTATCTATGCGCATTTTATCTTTATGCTGCTAGCCTTCTA 1020
 Db 961 GCCAAGTTTCTGCACTATCTATGCGCATTTTATCTTTATGCTGCTAGCCTTCTA 1020
 Qy 1021 GGTACAGTTTGAACATAAATAATCAATAAATGAAAGTAAATAATAGTTTATTTT 1080
 Db 1021 GGTACAGTTTGAACATAAATAATCAATAAATGAAAGTAAATAATAGTTTATTTT 1080
 Qy 1081 CATATTAAGTGGGATCATTTTGTAGATCAATCTGAATATTAATAAGCAATCTGATTT 1140
 Db 1081 CATATTAAGTGGGATCATTTTGTAGATCAATCTGAATATTAATAAGCAATCTGATTT 1140
 Qy 1141 TAAATACAAACCAATCTGCAAGGGAAGTCTATGATCGTGCAAGTGTGTTGAT 1200
 Db 1141 TAAATACAAACCAATCTGCAAGGGAAGTCTATGATCGTGCAAGTGTGTTGAT 1200
 Qy 1201 ATTCTTAGTCTAGATGGAGTCAAACTTTTAGTGCAAAATATCTATTAAGAAACCCCTA 1260
 Db 1201 ATTCTTAGTCTAGATGGAGTCAAACTTTTAGTGCAAAATATCTATTAAGAAACCCCTA 1260

RESULT 2

US-10-051-307-2

; Sequence 2, Application US/10051307

; Publication No. US20020170095A1

; GENERAL INFORMATION:

; APPLICANT: DAI, ZIYU

; APPLICANT: SHI, LIFANG

; APPLICANT: HOOKER, BRIAN S.

; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF

; FILE REFERENCE: 059440/0141

; CURRENT APPLICATION NUMBER: US/10/051.307

; PRIOR FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: 60/263,224

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 2

; TYPE: DNA

; ORGANISM: Solanum tuberosum

US-10-051-307-2

Query Match 92.9%; Score 1482.2; DB 14; Length 1598;

Best Local Similarity 96.7%; Pred. No. 0;

Matches 1546; Conservative 0; Mismatches 48; Indels 5; Gaps 3;

Qy 1 GTAATACGACTCACTATAGGCAACGCTGGTTCGACGCGCTGGTGTATCTTTGTTGA 60

Db 1 GTAATACGACTCACTATAGGCAACGCTGGTTCGACGCGCTGGTGTATCTTTGTTGA 60

Qy 61 AAAAATGGAAAAAGAACGCTAGGACCAATGGAACCTGGGTGCAACAATATGTTGCTC 120

Db 61 AAAAATGGAAAAAGAACGCTAGGACCAATGGAACCTGGGTGCAACAATATGTTGCTC 120

Qy 121 CAATATGGTACAGGATTTGTATCATCTCCGGTACTTTAAGTTGACCGGCAATTCAC 180

Db 121 CAATATGGTACAGGATTTGTATCATCTCCGGTACTTTAAGTTGACCGGCAATTCAC 180

Qy 181 CATTTATATTTGGCGTGCATTTGTTGGCAATTTCCCTCCACTTTGGATTAGTCGGGG 240

Db 181 CATTTATATTTGGCGTGCATTTGTTGGCAATTTCCCTCCACTTTGGATTAGTCGGGG 240

Qy 241 CGAAGTCATCGGTATATTAATTAATCCATCACTAAAGAAATGTCGCAAAATCTAAGTTGT 300

Db 241 CGAAGTCATCGGTATATTAATTAATCCATCACTAAAGAAATGTCGCAAAATCTAAGTTGT 300

Qy 301 TGAAGTCTGTCGCAAGGCTACTCGGCTAGGCTGTTGGTGGTTTGGCCCAACCCGTCAC 360

Db 301 TGAAGTCTGTCGCAAGGCTACTCGGCTAGGCTGTTGGTGGTTTGGCCCAACCCGTCAC 360

Applicant

Db 301 TGAACCTGGTCAAGGCGTACTCGGCTAGGGTGTGTTGGTGTGTTGGCCCAACCGGTCGACT 360
 Qy 361 GCAGGACACCAACCAATCAGCTGATGACGAACTCTACAGACCACTCAAGTTAC 420
 Db 361 GCAGGACACCAACCAATCAGCTGATGACGAACTCTACAGACCACTCAAGTTAC 420
 Qy 421 ATCCAGTACGACCCCATATACCTGCGATGCTAGTGGCCCTTAGGGGATCAATGACCCACA 480
 Db 421 ATCCAGTACGACCCCATATACCTGCGATGCTAGTGGCCCTTAGGGGATCAATGACCCACA 480
 Qy 481 TTTGGCCCGGATCAAAAGCTGGGACCGCTTTTCGGGGTCTGATCCGCCCAAAAGATGTA 540
 Db 481 TTTGGCCCTGATCAGAGCTGGGACCGCTCTATCGGGTCTGATCCGCCCAAAAGATGTA 540
 Qy 541 TGACAGTGTGTC--CGTACCTGATGTCGACGATAGTGAAGTCACAAAAGCAAGA 598
 Db 541 TGACAGTGTGTCGGGTGATCTGATGTCGACGATAGTGAAGTCACAAAAGCCAGA 600
 Qy 599 AGGAGAGAAACAAAGAGATCTCAAGTACGACCCATGTTTGTGAATTTATATGTGACA 658
 Db 601 AGGAGAGAAACAAAGAGATCTCAAGTACGACCCATGTTTGTGAATTTATATGTGACA 660
 Qy 659 AATTATTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCACTACGGATATTAAT 718
 Db 661 AATTATTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCACTACGGATATTAAT 720
 Qy 719 CGTATTATAGCAATATACATCTTGAATTAATTAACGAAATATATACATATGAT 778
 Db 721 CGTATTATAGCAATATACATCTTGAATTAATTAACGAAATATATACATATGAT 780
 Qy 779 TTGTTAAACGTTGAGGTGGAATAATGATTAAGACCGCTTAATTAATTAATTTATGA 838
 Db 781 TTGTTAAACGTTGAGGTGGAATAATGATTAAGACCGCTTAATTAATTTATGA 840
 Qy 839 ATATAGCTATAGTTACAAGTTAACTTTATTTGGTGAATACTTTGACATATAACTCTGT 898
 Db 841 ATATAGCTATAGTTACAAGTTAACTTTATTTGGTGAATACTTTGACATATAACTCTGT 900
 Qy 899 AACGTGACGGAATTTTCTTAAACTAAATATTAAGACGCTATTTTCAGATTTTTCG 958
 Db 901 AACGTGACGGAATTTTCTTAAACTAAATATTAAGACGCTATTTTCAGATTTTTCG 960
 Qy 959 TGGCCAAAGTTCTTGCACTACTATGATGCCATTTTACTTTTATCGTTCTAGCCTTC 1018
 Db 961 TGGCCAAAGTTCTTGCACTACTATGATGCCATTTTACTTTTATCGTTCTAGCCTTC 1020
 Qy 1019 TAGGTACACGTTTGAACATATAAAATCATATAAATTCGAAGTAAATTTAGTTTTCG 1078
 Db 1021 TAGGTACACGTTTGAACATATAAAATCATATAAATTCGAAGTAAATTTAGTTTTCG 1080
 Qy 1079 TTTCAATTTACTCGTAGGATCATTTGTTAGATCAATCTGAAATATACAAACCACTCTGAT 1138
 Db 1081 TTTCAATTTACTCGTAGGATCATTTGTTAGATCAATCTGAAATATACAAACCACTCTGAT 1140
 Qy 1139 TTTAAATATCAACCAATCTGCC--AGGGGAAGTCTATGATCCGTGCAAGTGTTTT 1196
 Db 1141 TTTAAATATCAACCAATCTGCCAAATGGGGAAGTCTATGATTCGTGGCAAGT-GTTT 1199
 Qy 1197 GATTATTTCTAGTCTAGATTCGAGTCAACCTTTTGTGCAAAATCTATTTAAAGAAC 1256
 Db 1200 GATTATTTCTAGTCTAGATTCGAGTCAACCTTTTGTGCAAAATCTATTTAAAGAAC 1259
 Qy 1257 CCTATTGATGCAAAATATCTATTAAGAACCCCTTATTCATGCTTTTATTTTACGAT 1316
 Db 1260 CCTATTGATGCAAAATATCTATTAAGAACCCCTTATTCATGCTTTTATTTTACGAT 1319
 Qy 1317 CGGAGCATGGATATATTTACTTAATTAATTAATTAAGGAATTTGATGCAAGTATC 1376
 Db 1320 CGGAGCATGGATATATTTACTTAATTAATTAATTAAGGAATTTGATGCAAGTATC 1379
 Qy 1377 AAGCTTATCGTCGATCCACATATAAATAACGTTAGTATGCTGCTTTTATAGGAAACAAAT 1436
 Db 1380 AAGCTTATCGTCGATCCACATATAGATTAACGTTAGTATGCTGCTTTTATAGGAAACAAAT 1439

Qy 1437 GGATCATGTATTAATTTAGTTTAAATATCTCTATAAATATCTATATATATCTCTCTAAA 1496
 Db 1440 GGATCATGTATTAATTTAGTTTAAATATCTCTATAAATATCTCTATCTCTCTAAA 1499
 Qy 1497 CTAAATGCATCTAAACAACAATATTAACCTTAGATTCTTTAAAGAAATTCAGAAATTA 1556
 Db 1500 CCAATATACATCTAAACAACAATATTAACCTTAGATTCTTTAAAGAAATTCAGAAATTA 1559
 Qy 1557 ATGGAGGCAATTAAGTCTATGTTGAAGTTGGTTGCTTTC 1595
 Db 1560 ATGGAGGCAATTAAGTCTATGTTGAAGTTGGTTGCTTTC 1598

RESULT 3

US-10-051-307-3
 ; Sequence 3, Application US/10051307
 ; Publication No. US20020170095A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DAI, ZIYU
 ; APPLICANT: SHI, LIFANG
 ; APPLICANT: HOOKER, BRIAN S.
 ; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
 ; FILE REFERENCE: 059440/0141
 ; CURRENT APPLICATION NUMBER: US/10/051,307
 ; CURRENT FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: 60/263,224
 ; PRIOR FILING DATE: 2001-01-23
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 1546
 ; TYPE: DNA
 ; ORGANISM: Solanum tuberosum
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (1248)
 ; OTHER INFORMATION: a, t, c or g
 US-10-051-307-3

Query Match 85.4%; Score 1362.4; DB 14; Length 1546;
 Best Local Similarity 94.1%; Pred. No. 3.2e-293;
 Matches 1460; Conservative 0; Mismatches 82; Indels 9; Gaps 4;

Qy 49 ATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACCAATGACCTTGGGTGCAACAAT 108
 Db 1 ATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACCAATGACCTTGGGTGCAACAAT 50
 Qy 109 ATTGTTGCTCTCCAAATGTGTACAAAGGATGTTACATCTCCGGGTACTTTAAGTTGAC 168
 Db 61 ATTGTTGCTCTCCAAATGTGTACAAAGGATGTTACATCTCCGGGTACTTTAAGTTGAC 120
 Qy 169 CAGGGCATTCACCATTTATTTGCGGTGCAATTTGTTGGCATTTCCCTCCACTTG 228
 Db 121 TAGGCATTCACCATTTATTTTGGGTGCAATTTGTTGGCATTTCCCTCCACTTG 180
 Qy 229 GATTAGTCCGGGCGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAAATGTCCACA 288
 Db 181 GATTAGTCCGGGCGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAAATGTCCACA 240
 Qy 289 AATCTAAGTTGTTGAACCTGCTCAGGGGTACTCGGTAGGTTGTTGGTTGGTCCGCC 348
 Db 241 AATCTAAGTTGTTGAACCTGCTCAGGGGTACTCGGTAGGTTGTTGGTTGGTCCGCC 300
 Qy 349 ACCGGGTGCACTGCGAGGACCAACCAATCACCAGTCAATGCAACCACTCTACAGACAC 408
 Db 301 ACCGGGTGCACTGCGAGGACCAACCAATCACCAGTCAATGCAACCACTCTACAGACAC 360
 Qy 409 CATCGAAGTTACATCCAGTACGACCCCAATATACCTGTCGATCGTATGCCCCCTAGGCGCAT 468
 Db 361 CATCGAAGTTACATCCAGTACGACCCCAATATACCTGTCGATCGTATGCCCCCTAGGCGCAT 420
 Qy 469 CAATGACCCACATTTGGCCCCGATCGAAACGTCGG-CACCCGCTTTTCGGGGTCGATGCCG 527

APR 18

Db 421 CAAATGACCCAGCTTGGCTCGATCGAGAGCTCGGCCACCGCTATCGGGTCTGATGCTG 480
 QY 528 CCCAAAGCGATGATGAGCAGTTTGGTACCTCGATGAGTGGGAGCAGTAAAGTCA 587
 Db 481 CCCAGACGGTGTATGAGCAGTTTGGTACCTCGATGAGTGGGAGCAGTAAAGTCA 540
 QY 588 CAAAAGCAAGAGGAGAGAAACAAAAGAGATCTCAAGTAGGCCATGTTTGGTGAATTT 647
 Db 541 CAAAAGCAAGAGGAGAGAAACAAAAGAGATCTCAAGTAGGCCATGTTTGGTGAATTT 600
 QY 648 ATATGTGGACAATTTTGGTACCTTTATATATAGGGATGAGGGCTTTGGGACAT 707
 Db 601 ATATGTGGACAATTTTGGTACCTTTATATATAGGGATGAGGGCTTTGGGACAT 660
 QY 708 CGGATATTAAATCGTATTATATAGCAATATCATCTTTGACTTAATTAACGAAATATAT 767
 Db 661 TGGATATTAAATCGTATTATATACAAATATCATCTTTGACTTAATTAACGAAATATAT 720
 QY 768 TACAATATGATTTGGTAAACGTTGAGTGGAAATATATAGAGCGCGCTAAATATA 827
 Db 721 TACAATATGATTTGGTAAACGTTGAGTGGCAAAATGATAGAGCGCGCTAAATATA 780
 QY 828 TTATTTTATGAATAGCTATAGTACAAGTTTAACTTTATTTGGTGAATCTTGACAT 887
 Db 781 TTATTTTATGAATAGCTATAGTACAAGTTTAACTTTATTTGGTGAATCTTGACAT 840
 QY 888 ATAACTCTGTAACTGACGGAATTTTCTTAAACTTAAATATAAAGAGCAGCTATTT 947
 Db 841 ATAACTCTGTATCGTGACGGAATTTTCTTAAACTTAAATATAAAGAGCAGCTATTT 900
 QY 948 CAGATTTTCTGTGCGCAAGTTTCTGCACTATCTATCTATGCGCATTTTATCTG 1007
 Db 901 AATATTTTCTGTGCGCAAGTTTCTGCACTATCTATCTATGCGCATTTTATCTG 960
 QY 1008 TTCTAGCTCTCTAGGTACAGCTTTGAACATAAATAATCATAAATTTGAAGTAAATTT 1067
 Db 961 TTCTAGCTCTCTAGGTACAGCTTTGAACATAAATAATCATAAATTTGAAGTAAATTT 1020
 QY 1068 AGTTTTTTTTTCAATATCTGATGAGGATCAATTTGTTAGTCAATCTGAATATACAA 1127
 Db 1021 AG---TTTTTTTTTCAATATCTGATGAGGATCAATTTGTTAGTCAATCTGAATATACAA 1077
 QY 1128 ACCATCTGATTTTAAATCACAACATCTGCGAAGGGAAGTCTAT--GTGATCCGT 1184
 Db 1078 ATCATCTGATTTTAAATCATACTATCTGATGAGGGAAGTCTATGTTGATCTG 1137
 QY 1185 GACAAGTGGTTGATTTCTTAGTCTGATGAGTCAACATTTTATGTCGAATATCT 1244
 Db 1138 GACAAGTGGTTGATTTCTTAGTCTGATGAGTCAACATTTTATGTCGAATATCT 1197
 QY 1245 ATTAAGAGACCCCTATTTGATGCAATATCTATTAAGAGACCCCTATTTATCTTTAT 1304
 Db 1198 ATTAAGAGACCCCTATTTGATGCAATATCTATTAAGAGACCCCTATTTATCTTTAT 1255
 QY 1305 TATTTTACGATCGGAGCATGATATATTTTACTTAATTAATAATTTGAAGGAATTTGAT 1364
 Db 1256 TATTTTACGATCGGAGCATGATATATTTTACTTAATTAATAATTTGAAGGAATTTGAT 1315
 QY 1365 CGCAAGTCAATCAAGCTTATCGTCAATCAATTAATAATTTGAAGGAATTTGAT 1424
 Db 1316 CGCAAGTCAATCAAGCTTATCGTCAATCAATTTCCCTTAAAGTATGAGTCTTTT 1375
 QY 1425 AGAAGAACAGTGGATCATCTATAATTTAGTTTAAATATCTTAAATATCTATAT 1484
 Db 1376 AGAAGAACAGTGGATCATCTATAATTTAGTTTAAATATCTTAAATATCTATAT 1435
 QY 1485 ATACCTCTAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1544
 Db 1436 ATACCTCTAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1495
 QY 1545 TTGAGAAATTAATTTGAGGAGCAATTAAGTCTATGTTGAAGTTGGTCTCTTTC 1595

Db 1496 TTGCAAAATTAATGAGGCAAAATAGTCTATGTTGAAGTTGTTGCTTTC 1546

RESULT 4
 US-10-341-961A-371/c
 ; Sequence 371, Application US/10341961A
 ; Publication No. US20040006787A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
 ; APPLICANT: Crasta, Oswald
 ; APPLICANT: Swirsky, Peter
 ; APPLICANT: Mysore, Kiran
 ; APPLICANT: Folkerts, Otto
 ; APPLICANT: Martin, Gregory
 ; APPLICANT: Ekengren, Sophia
 ; TITLE OF INVENTION: PLANT DEPENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGE
 ; TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE
 ; FILE REFERENCE: BTI.67A2
 ; CURRENT APPLICATION NUMBER: US/10/341.961A
 ; PRIOR FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: 60390249
 ; PRIOR FILING DATE: 2002-06-20
 ; PRIOR APPLICATION NUMBER: 60261029
 ; PRIOR FILING DATE: 2001-01-11
 ; PRIOR APPLICATION NUMBER: 60348792
 ; NUMBER OF SEQ ID NOS: 395
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 371
 ; LENGTH: 510
 ; TYPE: DNA
 ; ORGANISM: Lycopersicon esculentum
 ; US-10-341-961A-371

Query Match 18.4%; Score 293.4; DB 16; Length 510;
 Best Local Similarity 78.5%; Pred. No. 3.3e-55;
 Matches 351; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 49 ATCTTTGTTTGAATAATTTGAAAAAGACGTAGACACACATGGACCTTGGTGGCAACAT 108
 Db 448 ATCTTTGTTTGAATAATTTGAAAAAGACGTAGACACACATGGACCTTGGTGGCAACAT 389
 QY 109 ATTGTTGTCCTCCAAATGTTGTACAAAGATTGTTTACATCTCCGGGTACTTTAAGTTGAC 168
 Db 388 ATTGTTGTCCTCCAAATGTTGTACAAAGATTGTTTACATCTCCGGGTACTTTAAGTTGAC 329
 QY 169 CAGGCAATTCACCAATTTATATTTGCCGTGCAATGAAATGTTGTTGTCATTTCCCTCCATTG 228
 Db 328 CAGGCAATTCACCAATTTATATTTGGCTGTGCAATGAAATGTTGTTGTCATTTTCCAGGGCCAG 269
 QY 229 GATTAGTCGGGGCAAGTCAATCGGTATATTAATCCATCAACTAAAGAAATGTTCCAGCA 288
 Db 268 GCTTAGTTGGGCCCAAGACATAGGGATGTTGAATCCATCAATTAACAGAAATATCCCAAA 209
 QY 289 AATCTAAGTTGTTGAACTGTTCCAAAGGCGTACTCGGTAGGGTGTGTTGGTGGTTTGGCCCC 348
 Db 208 AATCTAGTTTACCAAACTGGTTTCAAGCGTATTTCAGTAAAGTGTGTTGGTGGTTTACCCC 149
 QY 349 ACCGGTGCATGAGGACACCAACCAATCAGGATGTCAGGACCTTACCAGCAC 408
 Db 148 ATCTTTGCAATCAGGACCTCCACCAATCAGGATGTCAGGACCTTACCAGCAC 89
 QY 409 CATGAAAGTTACATCCAGTACGACCCCATATATCTGTCATCTAGTCCCTAGGCGCAT 468
 Db 88 CATCAAAGTTGCAATTTAGTACGACCCCAATATCGTGCAATTTTAGTGCCAGGTGGGCCCC 29
 QY 469 CAATGACCAATTTGGCCCCGGATCGA 495
 Db 28 AAAACCAACCACTCTGACCTCTCTCGA 2

RESULT 5

US-09-938-842A-2118/c
 ; Sequence 2118, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRI1300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 2118
 ; LENGTH: 735
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-2118

Query Match 12.3%; Score 195.6; DB 9; Length 735;
 Best Local Similarity 62.3%; Pred. No. 2.6e-33;
 Matches 365; Conservative 0; Mismatches 204; Indels 17; Gaps 3;
 Qy 46 GGTATCTTTGTTGAAAAAATTGGAAGAACGTAGGACCAATG-----GACCTTGGG 99
 Db 586 GGCATCTCTGCTTAAAGAAATCTTGAGTACTCAGTATCGTACATGATCCCTGACCGTTGC 527
 Qy 100 TGCACAAATATTGTGTCCTCCAAATGTGTCAAGAGTGTATACATCTCCGGTACTT 159
 Db 526 TACAACAGTATTGGTTGCTGCTGAATACAGTACAGGTTGTTGCATCCACCTGGGGCTC 467
 Qy 160 TAAGTTGACAGGCGATTCCACATTTATATTGCGGTGCAATGAAATGTGTGGCATTTCC 219
 Db 466 TCAACAGTTTGGACATTTGCTGTTTATGCTGCGGTACATAGTATCGATGGCAGTTC- 408
 Qy 220 CTCACATTGGAATAGTCGGGCGAAGTCATCGGTATATTAATCCATCAACTAAAGAA 279
 Db 407 -----GAACTAGTTGGGCTAAACTCCATGAGTATGTTAAATCCATCGACAAGTGAGA 356
 Qy 280 TGTCCTCGAATCTAAGTTGTTGAAGTGTGCTCAAGGCGTACTCGGTAGGGTGTTCGGTG 339
 Db 355 TATCGTAGAAGTCTAAGTTGTTGAATGTTGTTCAAGCGTACTCAGCAACGTTTGGTG 296
 Qy 340 GTTTGCCCCACCCCGTGCACCTGACGACCAACCAATCAACAGTATGATCGACCACTC 399
 Db 295 GCTGTCCCGCCAGCTACATTTGGAGTCCACACTGCACTGCACTGCACTGCGCATCGGCCAC 236
 Qy 400 TACAGCACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCTAGTGTGCCCC 459
 Db 235 GACCTGAGAGTCAAAAGTTACAAATGGTCTTACCCCAATCCGTCGCAATTTAGTGGCCG 176
 Qy 460 TAGCGCATCAATGACCCCAATTTGGCCCGCATCGAAACGTGCGCACCCCGCTTTCCGGGT 519
 Db 175 CCGGACATCTAGCTCCATGATTTGGCCAGCATCTAGACGTGCG--CCACCTCCAGGGCT 118
 Qy 520 CGATGCGCCCAACAGTATGAGACAGTTGTTGCTACCTCGATAGTGGCAGCATAGT 579
 Db 117 TCGCGCAGCCACACCGGTAACTACATTTGGTTAGGATTTTCGAATGTGGCGGCTGTTC 58
 Qy 580 GAAAGTCAAAAGCAAGGAGGAGAGAAACAAAGAGATCTCAAG 625
 Db 57 GGTGAGATGAGCAAAAGTGGGAAATATGAAAGTAGAGACCAAG 12

RESULT 6
 US-09-938-842A-2118/c

; Sequence 2118, Application US/09938842A
 ; Publication No. US20040009476A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRI1300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 2118
 ; LENGTH: 735
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-2118

Query Match 12.3%; Score 195.6; DB 11; Length 735;
 Best Local Similarity 62.3%; Pred. No. 2.6e-33;
 Matches 365; Conservative 0; Mismatches 204; Indels 17; Gaps 3;
 Qy 46 GGTATCTTTGTTGAAAAAATTGGAAGAACGTAGGACCAATG-----GACCTTGGG 99
 Db 586 GGCATCTCTGCTTAAAGAAATCTTGAGTACTCAGTATCGTACATGATCCCTGACCGTTGC 527
 Qy 100 TGCACAAATATTGTGTCCTCCAAATGTGTCAAGAGTGTATACATCTCCGGTACTT 159
 Db 526 TACAACAGTATTGGTTGCTGCTGAATACAGTACAGGTTGTTGCATCCACCTGGGGCTC 467
 Qy 160 TAAGTTGACAGGCGATTCCACATTTATATTGCGGTGCAATGAAATGTGTGGCATTTCC 219
 Db 466 TCAACAGTTTGGACATTTGCTGTTTATGCTGCGGTACATAGTATCGATGGCAGTTC- 408
 Qy 220 CTCACATTGGAATAGTCGGGCGAAGTCAATCGGTATATTAATCCATCAACTAAAGAA 279
 Db 407 -----GAACTAGTTGGGCTAAACTCCATGAGTATGTTAAATCCATCGACAAGTGAGA 356
 Qy 280 TGTCCTCGAATCTAAGTTGTTGAAGTGTGCTCAAGGCGTACTCGGTAGGGTGTTCGGTG 339
 Db 355 TATCGTAGAAGTCTAAGTTGTTGAATGTTGTTCAAGCGTACTCAGCAACGTTTGGTG 296
 Qy 340 GTTTGCCCCACCCCGTGCACCTGACGACCAACCAATCAACAGTATGATCGACCACTC 399
 Db 295 GCTGTCCCGCCAGCTACATTTGGAGTCCACACTGCACTGCACTGCACTGCGCATCGGCCAC 236
 Qy 400 TACAGCACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCTAGTGTGCCCC 459
 Db 235 GACCTGAGAGTCAAAAGTTACAAATGGTCTTACCCCAATCCGTCGCAATTTAGTGGCCG 176
 Qy 460 TAGCGCATCAATGACCCCAATTTGGCCCGCATCGAAACGTGCGCACCCCGCTTTCCGGGT 519
 Db 175 CCGGACATCTAGCTCCATGATTTGGCCAGCATCTAGACGTGCG--CCACCTCCAGGGCT 118
 Qy 520 CGATGCGCCCAACAGTATGAGACAGTTGTTGCTACCTCGATAGTGGCAGCATAGT 579
 Db 117 TCGCGCAGCCACACCGGTAACTACATTTGGTTAGGATTTTCGAATGTGGCGGCTGTTC 58
 Qy 580 GAAAGTCAAAAGCAAGGAGGAGAGAAACAAAGAGATCTCAAG 625
 Db 57 GGTGAGATGAGCAAAAGTGGGAAATATGAAAGTAGAGACCAAG 12

RESULT 7
 US-09-770-445-334/c
 ; Sequence 334, Application US/09770445

```
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gortlach, Jorn
; APPLICANT: An, Yong-Oiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L. P.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurbán, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334
; LENGTH: 950
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-334

Query Match      12.3%; Score 195.6; DB 9; Length 950;
Best Local Similarity 62.3%; Pred. No. 3e-33;
Matches 365; Conservative 0; Mismatches 204; Indels 17; Gaps 3;

Qy 46 GGTATCTTTGTTGAAAAAATCGAAAGAACCTAGACACATG-----GACCTTGGG 99
Db 594 GGCATCTCTGTTAAAGAACTTGGTACTCAGTATCGGTACATGATCCCTGACCCCTCG 535
Qy 100 TGCAACAATATTTGTTGCTCCAAATGTGTACAAAGATTGTACATCTCCGGGTACTT 159
Db 534 TAGACAGTATTTGTTGCTCTGAAATACAGTACACGGGTTGTTCATCCACCTGGGGCTC 475
Qy 160 TAAGTTGACAGGGCATTCACATTTATATTTCCGGTGCAATGAATGTGTGCAATTTCC 219
Db 474 TCAACAGTTTGGACATTTGTCCTTTATGTCCTCGGTACATAGTATCCGATGGCAGTTTC- 416
Qy 220 CTCACCTTGATTTAGTTCGGGGGAAAGTCACTCGGTATATTAATCCATCAACTAAGAAA 279
Db 415 -----GAACTAGTTGGGCTAAATCCATAGTATGTTAAATCCATGCAAGTGAGA 364
Qy 280 TGTCGCCAGAAATCTAAGTTGTTGAACTGGTCCAGGGGTACTCGGTAGGGTGTGTTGGTG 339
Db 363 TATCGTAGAAGTCTAAGTTGTTGAAATGTTTCAAGGGTACTCAGCCACGTTTGGTG 304
Qy 340 GTTTGCCCCACCGGTGCATCGCAGACACACCAATCAACAGTATGCAAGAACCTC 399
Db 303 GCTGTCCCCAGCAGTACATTTGAGTCCACCACTGCAGTCAACAGTTTGGCATCGGCCAC 244
Qy 400 TACAGCACCATCGAAGTTACATCCAGTACGACCCCATATCTCGCATCTAGTGCCTCC 459
Db 243 GACCTGAGAGTCAAGTTTACATTTGTTCTACCCCAATCCGTGCAATTTAGTGCCTG 184
Qy 460 TAGCGCATCAATGACCAATTTGGCCCCGATTCGAAAGCTGTGGGCAACCGCTTTGGGGT 519
Db 183 CCGCGCATCTAGCTCCATGATTTGGCCAGCATCTAGACGTTCGG--CCACCTCCAGGGCT 126
Qy 520 CGATGCCGCCCAACAGATGTATGACAGTGTGTTGCGTACTCGATAGTGGCAGCATAGT 579

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 36321
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1956)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_WRT3847_132800C.1
US-10-424-599-36321

Query Match      10.8%; Score 173; DB 13; Length 1956;
Best Local Similarity 59.5%; Pred. No. 4.9e-28;
Matches 355; Conservative 0; Mismatches 225; Indels 17; Gaps 3;

Qy 45 TGGTATCTTTGTTGAAAAAATTCGAAAGAACCTAGACACCA-----TGGACCTTGG 98
Db 1338 TGGCACCTATCTTTGAAGAACCTTTGAGTAGTTTGTGGGCCACACAGCTTCTTGGCCATTG 1279
Qy 99 GTGCAACAATATTTGTTGCTCCAAATGTGTCAAGATTGTTACATCTCCGGGTACT 158
Db 1278 GTGACGCAATCTACTTCTGCTTTAAACACAGTGCAGGGGTTGTTCATCCCCAGGTGCC 1219
Qy 159 TTAAGTTGACCCAGGGCATTCACATTTATATTTGCGGTGCAATGAATGTGTGGCAATTC 218
Db 1218 CTTAATGCGCCCGGCGCATGCCCCATTCATATCAGCGCTGCAACTGATTTGTGTGACACCCA 1159
Qy 219 CCTCCACTGTGATTAGTCGGGGCGAAAGTCACTCGGTATATTAATCCATCAACTAAGAA 278
Db 1158 CC-----GTTTAGAGGTAGAGTCCATCGGAATGTTGAACCCGTCCACAAAGAG 1108
Qy 279 ATGTCGCCAGAAATCTAAGTTGTTGAACTGGTCCAGGCGTACTCGGTAGGGTGTGTTGGT 338
Db 1107 ATGTCGTAGAAATCTCGTTGCCAAATTTGTTTCAACGCAATTCGCAAGTGTGTTGGGA 1048
Qy 339 GGTTCGCCACCGGTGCATCGCAGGACACCAACAATCACCAGTCACTGACGAACT 398
Db 1047 GGGACCCCGGAGCTTGGCAATTTAGGCGCCCGGTGCGAGTCTCCCGTTTGGCAGCGGCGG 988
Qy 399 CTACGACCAACCATCGAAGTTTACATCCAGTACGACCCCATATATCTGCACTCGTAGTGCCT 458
Db 987 CGGCGGTGCGCATCAAGTTGCGCCCGTGGCGCCCATATACGGGCGCATGCGAGTGCCT 928
Qy 459 CTAGCGCATCAATGACCCACATTTGGCCCCGATTCGAAAGCTGTGGGACCCGCTTGGGG 518
Db 927 GGGTTACCCAGAGAGTTCCACGTTTGGCCACGCTCAGACGCGCGGCTCCAC--CCGGAC 870
Qy 519 TCGATGCGGCCCAACGATGTATGACAGTGTGTTGCGTACTCGATAGTGGCAGCATAG 578
```

Db 869 TCGCGGCGCCACACCGTGTAGGGCAATTGTTGACATCTCGAAGTTTGCAGCATGTA 810
 Qy 579 TGAAGTCAAAAAGCAAGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATGT 635
 Db 809 TTGTTGCCAAAGGTAAGGCCAACGTTAGCAGAGACAGTGCACAGTAAACCATTT 753

RESULT 9

US-10-636-396-4/c

; Sequence 4, Application US/10636396
 ; Publication No. US20040073971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Crasta, Oswald R.
 ; APPLICANT: Duwick, Jon
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guihua
 ; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
 ; FILE OF INVENTION: Genes and their Uses
 ; FILE REFERENCE: 5718-90
 ; CURRENT APPLICATION NUMBER: US/10/636,396
 ; CURRENT FILING DATE: 2003-08-07
 ; PRIOR APPLICATION NUMBER: US/09/589,733C
 ; PRIOR FILING DATE: 2000-06-08
 ; PRIOR APPLICATION NUMBER: 60/140,646
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/162,904
 ; PRIOR FILING DATE: 1999-11-01
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 875
 ; TYPE: DNA
 ; ORGANISM: Helianthus annuus
 ; US-10-636-396-4

Query Match 10.7%; Score 170.4; DB 12; Length 875;
 Best Local Similarity 59.7%; Pred. No. 1.2e-27;
 Matches 325; Conservative 0; Mismatches 211; Indels 8; Gaps 2;

Qy 49 ATCTTTGTTTGAAGAAATGGAAAGACGATGACACATGACCTTGGGTGCAACAAT 108
 Db 577 ATCTGCTTGAAGAAACCTTGATTAATCAGTTGTTCACATTTCCAGATTTGCAACAAT 518
 Qy 109 ATTGTGTCTCCAAATGTGTACAGGATTTTACATCTCCGGGTACTTTAAGTTGAC 168
 Db 517 ACTGATCAGTTTGTACACGGTGAAGGTTATTGACCCGCCAGGAGCCGTAACACAC 458
 Qy 169 CAGGCAATCACCATTATTTTCCGTGCAATGAATTTGTGCAATTTCCCTCCACTTG 228
 Db 457 CAGGACACTGGCCATTGATATCCGACGATACATGATACCCCGGTGCACCC-----AT 404
 Qy 229 GATTAGTCGGGGCGAAAGTCAATCGGTATATTAAATCCATCACTAAAGAAATGTCCAG 288
 Db 403 TAGAATTTGGTCTAAACACCATCGGCATTTGATCGTCCACAAAGAAATGTCAAGA 344
 Qy 289 AATCTAAGTTGTGAATCTGGTCAAGGCTACTCGGTAGGGTGTGTTGGTGGTTCGCC 348
 Db 343 AATCAAGATTGTGAATCTGGTCAAGGCTACTCGGCCAATGTGTGGGTGGGTACCAT 284
 Qy 349 ACCGGTGCATCGAGGACACCAACATCACCAGTCAATGACGAACCTTACCCAGCAC 408
 Db 283 AGTTTGGCATTTGGAGAGACCGTTGCAATCACCAGTCTGACCTGCTCGCCAGAAC 224
 Qy 409 CATCGAAGTTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTCCCTTAGGCGCAT 468
 Db 223 CATCAAGTTTGAATTTGTTCCGGGCCATATACGGGCTCCTGCTGCGAGTCCGACGG 164
 Qy 469 CAATGACCCCATTTGGCCCCGATCGAAGACGTCGGCACCCTTTCGGGGTCGATCGGC 528
 Db 163 TTAAGACACCGTTTGGCCTGAGTTAAGTTGTGCGCGCCAC--CAGGCACCGCACCGC 106
 Qy 529 CCAACGATGTGACACAGTTGTTGCGTACCTCGATAGTGGCAGCATAAAGTGAAGTCA 589

Db 105 CCRAACGGTGTATGACAGTGTTCGATATAGTGAACACGGCTGCTATATATGAAA 46
 Qy 589 AAAA 592
 Db 45 AAGA 42

RESULT 10

US-10-636-026-4/c
 ; Sequence 4, Application US/10636026
 ; Publication No. US2004011761A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Crasta, Oswald R.
 ; APPLICANT: Duwick, Jon
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guihua
 ; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
 ; FILE OF INVENTION: Genes and their Uses
 ; FILE REFERENCE: 5718-90
 ; CURRENT APPLICATION NUMBER: US/10/636,026
 ; CURRENT FILING DATE: 2003-08-07
 ; PRIOR APPLICATION NUMBER: US/09/589,733C
 ; PRIOR FILING DATE: 2000-06-08
 ; PRIOR APPLICATION NUMBER: 60/140,646
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/162,904
 ; PRIOR FILING DATE: 1999-11-01
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 875
 ; TYPE: DNA
 ; ORGANISM: Helianthus annuus
 ; US-10-636-026-4

Query Match 10.7%; Score 170.4; DB 17; Length 875;
 Best Local Similarity 59.7%; Pred. No. 1.2e-27;
 Matches 325; Conservative 0; Mismatches 211; Indels 8; Gaps 2;

Qy 49 ATCTTTGTTTGAAGAAATGGAAAGACGATGACACATGACCTTGGGTGCAACAAT 108
 Db 577 ATCTGCTTGAAGAAACCTTGATTAATCAGTTGTTCACATTTCCAGATTTGCAACAAT 518
 Qy 109 ATTGTGTCTCCAAATGTGTACAGGATTTTACATCTCCGGGTACTTTAAGTTGAC 168
 Db 517 ACTGATCAGTTTGTACACGGTGAAGGTTATTGACCCGCCAGGAGCCGTAACACAC 458
 Qy 169 CAGGCAATCACCATTATTTTCCGTGCAATGAATTTGTGCAATTTCCCTCCACTTG 228
 Db 457 CAGGACACTGGCCATTGATATCCGACGATACATGATACCCCGGTGCACCC-----AT 404
 Qy 229 GATTAGTCGGGGCGAAAGTCAATCGGTATATTAAATCCATCACTAAAGAAATGTCCAG 288
 Db 403 TAGAATTTGGTCTAAACACCATCGGCATTTGATCGTCCACAAAGAAATGTCAAGA 344
 Qy 289 AATCTAAGTTGTGAATCTGGTCAAGGCTACTCGGTAGGGTGTGTTGGTGGTTCGCC 348
 Db 343 AATCAAGATTGTGAATCTGGTCAAGGCTACTCGGCCAATGTGTGGGTGGGTACCAT 284
 Qy 349 ACCGGTGCATCGAGGACACCAACATCACCAGTCAATGACGAACCTTACCCAGCAC 408
 Db 283 AGTTTGGCATTTGGAGAGACCGTTGCAATCACCAGTCTGACCTGCTCGCCAGAAC 224
 Qy 409 CATCGAAGTTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTCCCTTAGGCGCAT 468
 Db 223 CATCAAGTTTGAATTTGTTCCGGGCCATATACGGGCTCCTGCTGCGAGTCCGACGG 164
 Qy 469 CAATGACCCCATTTGGCCCCGATCGAAGACGTCGGCACCCTTTCGGGGTCGATCGGC 528
 Db 163 TTAAGACACCGTTTGGCCTGAGTTAAGTTGTGCGCGCCAC--CAGGCACCGCACCGC 106

QY 529 CCAACAGATGATGACAGAGTTGTCGTACCTCATAGTGCAGCATAAGTGAAGTCAAC 588
Db |||||
QY 105 CCAACAGGTGATGACAGAGTTGTCGAATAGTGAACAGGCTGCAATGCTATAGTGAAA 46
Db |||||
QY 589 AAAA 592
Db |||||
QY 45 AAGA 42

RESULT 11

US-10-424-599-103619/c
; Sequence 103619, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hui-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 103619
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64586C.1
US-10-424-599-103619

Query Match 10.5%; Score 167; DB 13; Length 909;
Best Local Similarity 60.7%; Pred. No. 6.9e-27;
Matches 327; Conservative 0; Mismatches 205; Indels 7; Gaps 3;

QY 46 GGTATCTTTGTTGAAAAAATTGGAAAGAACGTAGGACACATGACCTGGTGGTCAAC 105
Db |||||
QY 631 GGCACCTTTGCTGAGAAATCTGGAATATCATGTGGCCACACGACTACCGAATTCAC 572
Db |||||
QY 106 AATATTGTTGCTCCAAATGTGGTACAGAGTTGTATACATCTCCGGGTACTTTAAGTT 165
Db |||||
QY 571 AGTACTGGTCGGTTTTGAAGACAGTGAAGGGTTGTGCAACCTCTTGAGTCTTTAGCT 512
QY 166 GACAGGGCATTCACCAATTTATTTTCCGCTGATGAAATGTGTGGCATTTTCCCTCCAC 225
Db |||||
QY 511 CACTAGGGCACTGTCCGTTAATGTCCGACGTGCA---GCTTATGCCACGTGTGCATCCAT 455
QY 226 TTGATTTAGTCGGGGCGAAAGTCACTCGGTATATTAAATCCATCAACTAAAGAAATGTCCC 285
Db |||||
QY 454 TCG---AGGTTGACTAAAGTCCATGGGCAGTTAAACCGTCGACGAGGAGATGTCGA 398
QY 286 AGAAATCTAAGTTGTAACCTGTCTCAAGCGTACTCGGCTAGGTTGTTGGTGGTTTGC 345
Db |||||
QY 397 AGAAGTCCAAATTTGTAACCCGTTTCAGGCGGTATTTCAGCCAGGGTGTGGGAGGCGCAC 338
QY 346 CCCACCCGGTGCATGACGAGACACACCAATCAACGATGACGACCACTCTACACAG 405
Db |||||
QY 337 CGTAAGCTTTGAGTGCAGAGACACCCCGCAGTCACTCGGTCTGGCATCCACCGGCGCG 278
QY 406 CACATCGAAGTTTACATCCAGTACGACCCCATATATCTGCGCATCTGTAGTGCCTTAGGGG 465
Db |||||
QY 277 AACCGTTCGAAGTTGACGCGGTTTCGGGCGCCCAACCGGGGCGCCCTTTCTGTCAGGCA 218
QY 466 CATCAATGACCCACATTTGGCCCCGATCGAAACGTCGGCACCGGCTTTTCGGGGTC-GATG 524
Db |||||
QY 217 CGTCCACGACCAATGATGCCCCGGGTTTAATTGACGACCAACCGCCACAGGACAGACG 158
QY 525 CCGCCCAACAGATGTATGACAGTTGTTCGGTACCTTCGATAGTGGCAGCATAAAGTGA 583
Db |||||
QY 157 CAGCCACAGACAGTGTATGTCATCGGTTTGTGATTTTCAAAACCTTGCAGCATATCGGAA 99

RESULT 12

US-10-259-165-389/c
; Sequence 389, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hui-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 389
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-389

Query Match 8.6%; Score 137.4; DB 15; Length 717;
Best Local Similarity 56.9%; Pred. No. 2.4e-20;
Matches 292; Conservative 0; Mismatches 216; Indels 5; Gaps 2;

QY 98 GGTGCAACAATATTGTTGTCCTCCAAATGTGGTACAAGGATTTGTATCATCTCCGGGTAC 157
Db |||||
QY 541 GGTGACAGTACTGTTCTGCTTGAACACCGTGCACGCGTGTGTGCACCGCGCGCGCGC 482
QY 158 TTTAAGTTGACACGGGCAATTCACCAATTTATTTTCCGTCGCTGATTAATTGTG---TGCC 213
Db |||||
QY 481 CCTAGCTCGTCGGGCACTGCCCCCGCACGTCGCGCTCGCACCGCGCGCGCCCTTGGC 422
QY 214 ATTTCCCTCCACTTTGGATTAGTCGGGGCGAAAGTCACTCGGTATATTAATTAATCCATCAACTA 273
Db |||||
QY 421 GCACCCGCGCGCTCGCGCGGGGAGGAAGTCCATGGGCACGTTGAATCCGTCGATGA 362
QY 274 AAGAAATGTCACCAAAATCTAAGTTGTGAAGTGTCAAGGCGTACTCGCTAGGCTGT 333
Db |||||
QY 361 GGGAGATGTGGAAGAAGTCGAGGTTGCTGAAGTGTGTTTCAGCGCGAACTCCGCCAGCGGTGT 302
QY 334 TTGTGTTGTTTCCCGCCACCCGCTGACATGTCAGGACACACCAACCAATCACTAGTATGCAAG 393
Db |||||
QY 301 TGGGCGGCTGCGCGTACGCGCGCACCGCGACGCGCGCGCGCTCGCGCTCTGAGACC 242
QY 394 AACCTCTACAGACACCATCGAAAGTTATCATCAGTACGACCCCATATATACCTGCGCATCTGTAG 453
Db |||||
QY 241 GCCCGTTGCGCTGCGCTCGAAGCTGACGCGCGCTGCGCGCGCGCGCGCGCGCGCTCG 182
QY 454 TGCCCCCTAGGCGCATCAATGACCCACATTTTGGCCCCGATCGAAACGTCGACCGCGC-CTT 512
Db |||||
QY 181 TGCGGCGCGCACGTCGATCACCATCTGTCGCCCGGCTCCAGTGTCTGCTGCTGCCCGCGCG 122
QY 513 TCGGGGTGATGCGCGCCCAAAACGATGTATGGAAGTGTGTTGCTGATCTCGATAGTGGCAG 572
Db |||||
QY 121 ACGCACGCGCTGCGCGCCACACGCTGATCTGGCACATTTGTTGTTGTTGTTGTTGTTGTTGTTG 62
QY 573 CATAAAGTGAAGTGCACAAAAGCAAGAGGAGA 605

Db 61 CGTTCGGCGCGCGGAGGAGGAGGAGGGA 29

RESULT 13

US-10-259-165-41/c
; Sequence 41, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 41
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-10-259-165-41

Query Match 8.6%; Score 137.4; DB 15; Length 720;
Best Local Similarity 56.9%; Pred. No. 2.4e-20;
Matches 292; Conservative 0; Mismatches 216; Indels 5; Gaps 2;
QY 98 GGTGCAACATATTGTTGCTCTCCAAATGGTACAGGATTGTTACATCTCCGGGTAC 157
DB 541 GGTGCAACATATTGTTGCTCTCCAAATGGTACAGGATTGTTACATCTCCGGGTAC 482
QY 158 TTTAAGTTGACAGGCAATTCACCAATTTATTTGCGGTGCAATTTGATTTGTG 213
DB 481 CCTCAGTCGTCGGGCACTGCCCCGCCACGTCGCTCGCACCGCGGCCCTTTGGC 422
QY 214 ATTTCCCTCCACTTTGGATTAGTCGGGGGAAAGTATCATCGGTATATTAAATCCATCAACTA 273
DB 421 GCACCCGCGCGCTCGCGCGGGGGAGGAAGTCCATGGGCACGTTGAATCCGTCGATGA 362
QY 274 AAGAATGTCACCAATTAAGTTGTTGAATCTGTCACAGGCGTACTCGGCTAGGGTGT 333
DB 361 GGGAGATGTCGAAGAAGTCGAGTTGCTGAACTGTTTCAAGCGCAATTCGCCAGCGTGT 302
QY 334 TTGGTGTGTTTCCCGCACCCCGGTGCACTGCAAGACACCAACCAATTCACAGTATGCAAG 393
DB 301 TGGCGGGCTGCGCGTACGCGCGCACCGCACGCGCGCGCGCGCTGCGCGCAC 242
QY 394 AACCTCTACAGCAGCATCGAAGTTATCATCCAGTACGACCCCATATACCTGCCATCGTAG 453
DB 241 GCCCGTTGCCCGTGCAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAG 182
QY 454 TGCCCTTAGGCGCATCAATGACCCACATTTGGCCCGCGATCGAAACGTCGGCACCGC-CTT 512
DB 181 TGCCCGCGGACGTCGATCACCCACATGCTGCTCCCGCGGTCCAGTGTGCTGCGCGCGG 122
QY 513 TCGGGGTGATGTCGCGCCCAACAGATGATGACAGATGTTGCGGTACCTCGATAGTGGCAG 572
DB 121 ACGGCACGCGCTGCGCGCCACACGCGTATCTGGCACTTTGTTGGTATGGTGAACGTGGCGG 62

QY 573 CATRAAGTGAAGTCAAAAAACAAGAGGGGAGA 605
DB 61 CGTTCGGCGCGCGGAGGAGGAGGAGGGA 29

RESULT 14

US-10-437-963-86607/c
; Sequence 86607, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 86607
; LENGTH: 1006
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MBT4530_85631C.1
; US-10-437-963-86607

Query Match 8.5%; Score 135.2; DB 17; Length 1006;
Best Local Similarity 56.6%; Pred. No. 9e-20;
Matches 290; Conservative 0; Mismatches 218; Indels 4; Gaps 2;

QY 98 GGTGCAACATATTGTTGCTCTCCAAATGGTACAGGATTGTTACATCTCCGGGTAC 157
DB 584 GGTGCAACATATTGTTGCTCTCCAAATGGTACAGGATTGTTACATCTCCGGGTAC 525
QY 158 TTTAAGTTGACAGGCAATTCACCAATTTATTTGCGGTGCAATTTGATTTGTG 214
DB 524 CCTCAGTCGTCGGGCACTGCCCCGCCACGTCGCTCGCACCGCGGCCCTTTGGC 465
QY 215 TTTCCCTCCACTTTGGATTAGTCGGGGGAAAGTATCATCGGTATATTAAATCCATCAACTAA 274
DB 464 GCACCCGCGCGCTCGCGCGGGGGAGGAAGTCCATGGGCACGTTGAATCCGTCGATGAG 405
QY 275 AAGAATGTCACCAATTAAGTTGTTGAATCTGTCACAGGCGTACTCGGCTAGGGTGT 334
DB 404 GGAGATGTCGAAGAAGTCGAGTTGCTGAACTGTTTACGCGGCACTCGCCAGCGGTGT 345
QY 335 TGGTGTGTTTCCCGCACCCCGGTGCACTGCAAGGACACCAACCAATTCACAGTATGCAAG 394
DB 344 GGGCGGCTGCCCGTACGCGCGCACCGCACGCGCGCGCGCGCTGCGCGCAC 285
QY 395 ACCTCTACAGCAGCATCGAAGTTATCATCCAGTACGACCCCATATACCTGCCATCGTACT 454
DB 284 CCGTTTGGCGTGCAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAG 225
QY 455 GCCCTTAGGCGCATCAATGACCCACATTTGGCCCGCGATCGAAACGTCGGCACCGC-CTTT 513
DB 224 GCGGCGGCGCAGTCGATCACCCACTGCTGCCCCGGGTCCAGTGTGCTGCGCGCGCGGA 165
QY 514 CGGGGTGATGTCGCGCCCAACAGATGATGACAGATGTTGCGGTACCTCGATAGTGGCAG 573
DB 164 CGGCACGCGTGCAGCGCCACACGCGTATCTGGCACTTTGTTGGTATGGTGAACGTGGCGGC 105
QY 574 ATAAGTGAAGTCAAAAAACAAGAGGGGAGA 605
DB 104 GTTCGCGCGCGCGGAGGAGGAGGAGGGA 73

Search completed: August 18, 2004, 16:52:35
Job time : 708.41 secs

RESULT 15
US-10-424-599-7736/c
; Sequence 7736, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 7736
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(1173)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_106998C.1
US-10-424-599-7736

Query Match 8.3%; Score 132; DB 13; Length 1173;
Best Local Similarity 57.0%; Pred. No. 5.1e-19;
Matches 311; Conservative 0; Mismatches 215; Indels 20; Gaps 3;

QY 49 ATCTTTGTTGAAATAATCGAAAGAACCTAGGACACACA-----TGGACCTTGGGTGC 102
DB 664 ACCTCTCTTTGAAGAACTTGGAAATATCATGTGGGACCGCAACCCGCGAGCACCGGTGCTAC 605

QY 103 AACAAATATCTGTCCTCCAAATGTGGTACAGGATGTGTACATCTCTCGGGTACTTTAA 162
DB 604 AACAGTACTGAGTCGTATTGTAACACCGTGACGGGTGTGTGACGGCGCGGAAACCTGAA 545

QY 163 GTTGACCGAGGGCATTCACCATTTATATTTCCGTGCATTGAATTTGTGGCATTTCCCTC 222
DB 544 GCTGAGTGGGACACTCTCCGATGATGTCCGGCGCGCATTTACGGAGCTGCAGTTG---- 489

QY 223 CACTTGAATTAGTCGGGGCGAAAGTCATCGGTATATTAATTCATCAACTAAGAAATGT 282
DB 488 -----TAGGTCCGGGCTCACCTGCAAGGGAATGTTGAACCGTCCGACGAGGAGATGT 437

QY 283 CCCAGAAATCTAAGTTGTTGAACCTGCTCAAGGCGTACTCGGTAGGGTGTGTTGGTGT 342
DB 436 CGTAGAGTCGAGGTTGTTGTACTGTTTCAACGGGAATTCACACAGTGTTCGGAGGTG 377

QY 343 TGCCCCACCCGGTGCACGTGAGGACACCAACAATCACCAAGTCATGACGAACCTCTAC 402
DB 376 TACCTGTTTGTGCACTCAAGAACACCCGTCGAGTCGCGGTGAGGCACTTCCCGCGTC 317

QY 403 CAGCACCATCGAAGTTACATCCAGTACGACCCCATATCTGCCATCGTAGTCCCTTAG 462
DB 316 CTGCGTTGTGCAAGGTGAGTTGTTGTCGACCCCAAGATGCGTCTCTCTGTCGTCGCTCG 257

QY 463 GCGCATCAATGACCCACATTTGGCCCGCATCGAAACGTCGGCACCCGCTTTTCGGGGTGA 522
DB 256 TCACGCTGATGTTCCACGATTCGCCAGGTTAAGCTTTGAGCCGCGC--CGGGCACGCGC 199

QY 523 TGCCGCCCAACGATGATGAGCAGTTGTTGGTACCTCGATAGTGGAGCAATAGTGAA 582
DB 198 GCGGCCCAACACCGTGTAGTGCAATTTGTTGATGTGTAAGTTGCTGCTGAGCTAC 139

QY 583 AGTCAC 588
DB 138 GGCCAC 133

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 03:35:10 ; Search time 6041.75 Seconds
(without alignments)
11442.406 Million cell updates/sec

Title: US-10-051-307-1
Perfect score: 1595
Sequence: 1 gtaataagactactatagg.....tggtaagtgtgtgtttc 1595

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
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- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1595	100.0	1595	6	AX665978	AX665978 Sequence
2	1482.2	92.9	1598	6	AX665979	AX665979 Sequence
3	1362.4	85.4	1546	6	AX665980	AX665980 Sequence
C 4	718.6	45.1	2659	8	SC81OLP	X72927 S.commerson
C 5	545	34.2	2638	8	SC13OLP	X72928 S.commerson
C 6	532	33.4	1304	8	AF933743	AF933743 Lycopersi
C 7	491	30.8	901	8	SCOSMLP	X67121 S.commerson
C 8	480.2	30.1	2033	8	NTOSPR	X95308 N.tabacum o
C 9	479.2	30.0	1549	8	NTAP24G	X65701 N.tabacum a
C 10	479.2	30.0	3033	6	ARQ37158	ARQ37158 Sequence
C 11	479.2	30.0	3033	8	S40046	S40046 abscisic ac
C 12	463.6	29.1	818	8	AY007309	AY007309 Solanum d
C 13	463.4	29.1	729	8	AF473702	AF473702 Solanum n
C 14	463.2	29.0	917	8	AY093595	AY093595 Lycopersi
C 15	463	29.0	744	8	AF450276	AF450276 Solanum n
C 16	460.2	28.9	977	8	SCA81OLP	X72926 S.commerson
C 17	458.6	28.8	937	8	AF297646	AF297646 Capsicum
C 18	456.4	28.6	856	8	CAN297410	AJ297410 Capsicum
C 19	438.6	27.5	832	8	LETMLM	X66416 L.esculentu
C 20	430.2	27.0	883	6	AL6780	AL6780 osmotin-lik
C 21	430.2	27.0	883	6	AR027097	AR027097 Sequence
C 22	430.2	27.0	883	6	AR103205	AR103205 Sequence
C 23	430.2	27.0	884	6	AL6782	AL6782 osmotin-lik
C 24	430.2	27.0	884	6	AR027098	AR027098 Sequence
C 25	430.2	27.0	884	6	AR103206	AR103206 Sequence
C 26	430.2	27.0	961	8	NTAP24	X65700 N.tabacum m
C 27	429.4	26.9	845	8	LEFRPA	X70787 L.esculentu
C 28	428.2	26.8	741	6	A83550	A83550 Sequence 1
C 29	428.2	26.8	741	6	BD082734	BD082734 Antifunga
C 30	424.4	26.6	928	8	S44889	S44889 osmotin=pat
C 31	421.4	26.4	917	8	TOMNP24	M21346 Tomato NP24
C 32	409.2	25.7	971	8	AF376058	AF376058 Petunia x
C 33	404.2	25.3	738	8	NTOSMOTIN	X61679 N.tabacum m
C 34	399	25.0	541	8	AY256440	AY256440 Solanum t
C 35	398.8	25.0	542	8	AY256441	AY256441 Solanum t
C 36	398.6	25.0	526	8	AY256436	AY256436 Solanum t
C 37	398.2	25.0	593	8	AY256429	AY256429 Solanum t
C 38	397.8	24.9	567	8	AY256439	AY256439 Solanum t
C 39	395	24.8	538	8	AY256431	AY256431 Solanum t
C 40	394.2	24.7	535	8	AY256434	AY256434 Solanum t
C 41	394	24.7	510	8	AY256425	AY256425 Solanum t
C 42	392.4	24.6	539	8	AY256430	AY256430 Solanum t
C 43	387.8	24.3	621	8	AF450277	AF450277 Solanum n
C 44	385.8	24.2	3127	8	TOBNP50	D76437 Nicotiana s
C 45	384.6	24.1	541	8	AY256428	AY256428 Solanum t

ALIGNMENTS

RESULT 1	AX665978	AX665978	1595 bp	DNA	linear	PAT 26-MAR-2003
LOCUS	AX665978	Sequence 1 from Patent WO02059333.				
DEFINITION	AX665978					
ACCESSION	AX665978					
VERSION	AX665978.1	GI:29290847				
KEYWORDS						
SOURCE		Solanum tuberosum (potato)				
ORGANISM		Solanum tuberosum				
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
		asterids; lamids; Solanales; Solanaceae; Solanum.				
REFERENCE 1						
AUTHORS		Dai, Z., Shi, L. and Hooker, B.S.				
TITLE		Gene promoters isolated from potato and use thereof				

Pred. No. is the number of results predicted by chance to have a

Query Match	92.9%;	Score 1482.2;	DB 6;	Length 1598;	
Best Local Similarity	96.7%;	Pred. No. 1.8e-285;			
Matches 1546;	Conservative	0;	Mismatches 48;	Indels 5;	Gaps 3;
QY	1	GTAATACGACTCACTATAGGCGACGCGTGTGCGACGCGCCCTGGCTGGTATCTTTGTTGA	60		
DB	1	GTAATACGACTCACTATAGGCGACGCGTGTGCGACGCGCCGCGTGTATCTTTGTTGA	60		
QY	61	AAAAATTTGAAAAAGAAAGTGGAGCCACATGACCTTGGGTGGCAACATATTTGTTGCTTC	120		
DB	61	AAAAATTTGAAAAAGAAAGTGGAGCCACATGACCTTGGGTGGCAACATATTTGTTGCTTC	120		
QY	121	CAAAATGTTGTACAAGGATTTTACATCTCCGGTACTTTAAGTTGACCGGCAATTCAC	180		
DB	121	CAAAATGTTGTACAAGGATTTTACATCTCCGGTACTTTAAGTGTGACTAGGACATTCAC	180		
QY	181	CATTATATTTGCGCTGCATTTGAATTTGTGGCATTTCCCTCCACTTTGGATTAAGTGGGG	240		
DB	181	CATTATATTTGCGCTGCATTTGAATTTGTGGCATTTCCCTCCACTTTGGATTAAGTGGGG	240		
QY	241	CGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCOCAGAAATCTAAGTTGT	300		
DB	241	CGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCOCAGAAATCTAAGTTGT	300		
QY	301	TGAATCGGTCCAGCGGTACTCGGCTAGGGTGTGTTGGTGTGTTGCCCCACCGGTGCACT	360		
DB	301	TGAATCGGTCCAGCGGTACTCGGCTAGGGTGTGTTGGTGTGTTGCCCCACCGGTGCACT	360		
QY	361	GCAGGACACCAACCAATCACCAGTCATGCAGCAACCTCTACAGCAGCACCAATCGAAGTTAC	420		
DB	361	GCAGGACACCAACCAATCACCAGTCATGCAGCAACCTCTACAGCAGCACCAATCGAAGTTAC	420		
QY	421	ATCCAGTACGACCCCATATACCTCCATPGGTAGTGGCCCTTAGGCGCATCAATGACCCACA	480		
DB	421	ATCCAGTACGACCCCATATACCTCCATPGGTAGTGGCCCTTAGGCGCATCAATGACCCACA	480		
QY	481	TTTGCGCCCGATCGAAGCGTGGCAGCCGCTTTGCGGGTGCATGCGCCGCAACGATGTA	540		
DB	481	TTTGCGCCCGATCGAAGCGTGGCAGCCGCTTTGCGGGTGCATGCGCCGCAACGATGTA	540		
QY	541	TGGACAGTTGTTG--CGTACCTCGATAGTGGCAGCATAGTGAAGTCAAAAAGCAAGA	598		
DB	541	TGGACAGTTGTTGCGGTGTTGCTGATAGTGAAGTGAAGTCAAAAAGCAAGA	600		
QY	599	AGGAGAGAAACAAAGAGATCTCAAGTACGCCATGTTGTTGAAATTTATATGTGACA	658		
DB	601	AGGAGAGAAACAAAGAGATCTCAAGTACGCCATGTTGTTGAAATTTATATGTGACA	660		
QY	659	AATTATTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCAGTACGGATATTAAT	718		
DB	661	AATTATTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCAGTACGGATATTAAT	720		
QY	719	CGTATATATAGCAATATCATCTTGTGACTAATTTATAAGCAATATATTAACAATATGAT	778		
DB	721	CGTATATATTAACAATATCATCTTGTGACTAATTTATAAGCAATATATTAACAATATGAT	780		
QY	779	TGCTTAACGTTGAGTGGGAAATATATAGAGCCGCTTAATTAATTTATTTATGA	838		
DB	781	TTGGTAAACGTTGAGTGGGAAATATATAGAGCCGCTTAATTAATTTATTTATGA	840		
QY	839	ATATAGCCTATAGTTACAAAGTTAACTTTATTTGGTGATACTTTGACATATAAATCTGT	898		
DB	841	ATATAGCCTATAGTTACAAAGTTAACTTTATTTGGTGATACTTTGACATATAAATCTGT	900		
QY	899	AACGTGACGGAATTTTCTTAAACTAAATATTAAGAGCGCTATTTTCAGATTTTCG	958		
DB	901	AACGTGACGGAATTTTCTTAAACTAAATATTAAGAGCGCTATTTTTCACATTTTTCG	960		
QY	959	TGGCCAAAGTTTCTTGCATCTTATCTATGCCATTTTATCTTTTATCGTTCTAGCCTTC	1018		
DB	961	TGGCCAAAGTTTCTTGCATCTTATCTATGCCATTTTATCTTTTATCGTTCTAGCCTTC	1020		
QY	1019	TAGTACACGTTTGAACATAAAAAATCATAAAAATGAAAGTAAAAATTAGTTTTTTTTT	1078		
DB	1021	TAGTACACGTTTGAACATAAAAAATCATAAAAATGAAAGTAAAAATTAGTTTTTTTTT	1080		
QY	1079	TTTCATATTACTCGTAGGATCATTTTGTAGATCAATCTGAATATACAAACCATCTGAT	1138		
DB	1081	TTTCATATTACTCGTAGGATCATTTTGTAGATCAATCTGAATATACAAACCATCTGAT	1140		
QY	1139	TTTAAATCACAACCATCTTGCC--AAGGGGAAGTCTATGTGATCCGTGACAAAGTGGTTT	1196		
DB	1141	TTTAAATCACAACCATCTTGCC--AAGGGGAAGTCTATGTGATCCGTGCGCAAGT-GTTT	1199		
QY	1197	GATTATCTTGTAGTGTGAGTACAACTTTTGTAGTGCATAATCTATTAAGAAGAAC	1256		
DB	1200	GATTATCTTGTAGTGTGAGTACAACTTTTGTAGTGCATAATCTATTAAGAAGAAC	1259		
QY	1257	CTATTGTATGCAAAATCTATTAAGAAAGACCCCTATTCATGCTTTATTTTATACGAT	1316		
DB	1260	CTATTGTATGCAAAATCTATTAAGAAAGACCCCTATTCATGCTTTATTTTATACGAT	1319		
QY	1317	CGAGCATGATATATTTACTAATTAATAAATAAATTTGGAAGGAATTCATGCAAGTCAATC	1376		
DB	1320	CGAGCATGATATATTTACTAATTAATAAATAAATTTGGAAGGAATTCATGCAAGTCAATC	1379		
QY	1377	AGCTTATCGTCGATCCCATTAATAACGTTAGTATGCTGCTTTTGTAGAGAAACAAGT	1436		
DB	1380	AGCTTATCGTCGATCCCATTAATAACGTTAGTATGCTGCTTTTGTAGAGAAACAAGT	1439		
QY	1437	GGATCATGTATTAATTTAGTTTAAATAATCTCTATAAATATCTATATATACCTCTAA	1496		
DB	1440	GGATCATGTATTAATTTAGTTTAAATAATCTCTATAAATATCTCTATACCTCTTAA	1499		
QY	1497	CTAATGTCATCTAACACCAATATTAACCTTAGATTCTTTTAAAGAAATTCAGAAATTA	1556		
DB	1500	CCAAATACATCTAACACCAAAATATAAATCTTAGATTCTTTTAAAGAAATTCAGAAATTA	1559		
QY	1557	ATGGAGGCAATAAAGTCTATGCTGAAGTTGGTTGCTTTC	1595		
DB	1560	ATGGAGGCAATAAAGTCTATGCTGAAGTTGGTTGCTTTC	1598		
RESULT 3					
LOCUS	AX665980	1546 bp	DNA	linear	PAT 26-MAR-2003
DEFINITION	Sequence 3 from Patent WO02059333.				
ACCESSION	AX665980				
VERSION	AX665980.1	GI:29290849			
KEYWORDS	Solanum tuberosum (potato)				
SOURCE	Solanum tuberosum				
ORGANISM	Solanum tuberosum (potato)				
REFERENCE	1 Dai, Z., Shi, L. and Hooker, B.S.				
AUTHORS	Gene promoters isolated from potato and use thereof				
TITLE	Patent: WO 02059333-A 3 01-AUG-2002;				
JOURNAL	Dai, Ziyu (US) ; Shi, Lifang (US) ; Hooker, Brian, S. (US)				
FEATURES	Location/Qualifiers				
source	1. .1546				
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Query Match	85.4%;	Score 1362.4;	DB 6;	Length 1546;	
Best Local Similarity	94.1%;	Pred. No. 1.4e-261;			
Matches 1460;	Conservative	0;	Mismatches 82;	Indels 9;	Gaps 4;
QY	49	ATCTTTGTTTGA AAAAATTTGAAAAAGACCTAGGACCAATGCGCTGGTGGCAACAT	108		
DB	1	AUCTTTGTTTGA AAAAATTTGAAAAAGACCTAGGACCAATGCGCTGGTGGCAACAT	60		
QY	109	ATTGTTGCTCTCCAAATGTTGTA CAAGATTTGATCCTCGGGTACTTTTAAAGTTGAC	168		


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Db      129  CCGCCCAACGCGTGTATCGACAGTTGTTGGTACCTCGATAGTGGCAGCATAGTGAAG 70
Qy      585  TCACAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGTGAA 643
Db      69  TCACAAAGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGTGAA 11

RESULT 8
NTOSPR/c
LOCUS   NTOSPR N.tabacum osmotin gene. 2033 bp DNA linear PLN 01-FEB-1996
DEFINITION N.tabacum osmotin gene.
ACCESSION X95308
VERSION X95308.1 GI:1167853
KEYWORDS osmotin; PR protein.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1
REFERENCE
AUTHORS Barnard,W.M. and Neale,A.D.
TITLE Comparison of the 5 regulatory regions of homeologous osmotin genes
from Nicotiana tabacum
JOURNAL Unpublished
AUTHORS Neale,A.D.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-1996) A.D. Neale, Monash University, Genetics and
Developmental Biology, Wellington Rd, Clayton, Victoria, 3168,
Australia
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 30.1%; Score 480.2; DB 8; Length 2033;
Best Local Similarity 76.9%; Pred. No. 1.3e-85;
Matches 679; Conservative 0; Mismatches 163; Indels 41; Gaps 6;
Qy 46 GGATCTTTTGGAAAAATTCGAAAGAACGTAGGACCATGGACCTCGGTGGCAAC 105
Db 1745 GGCATCTTTTGGAAAAATTTGAGAAAATGTAGGACCAAGTCTCTGTGGCAAC 1686
Qy 106 AATATTGTTGCTCTCCAAATGTGGTACAAAGATTGTATACATCTCCGGGTACTTTAAGTT 165
Db 1685 AATATTGTTGCTCTCCAAATGTAGTACAAAGGTTATTACATCTCCGGGAACCCCTAAGTT 1626
Qy 166 GACGAGGATTCACCATTTATTTGGCGTGCATGAATTGTGGGATTTCCCTCCAC 225
Db 1625 CTCGGGAGCATTCACCGTTTATATTGGCCGTGCAATGAATGCATGGCATTTCCCTCCAC 1566

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Qy      226  TTGGATTAGTGGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCC 285
Db      1565  TAGGGTTTAGTGGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCC 1506
Qy      286  AGAAATCTAAAGTTGTTGAACTGGTCCAGGCGTACTCGGTAGGTGTTTGGTGGTTGC 345
Db      1505  AAAATCTAAGCCCATGAATTGGTCCATGCGTATTGGCCCAAGGTGTTTGGTGGTTAC 1446
Qy      346  CCCACCCGGTGCACCTGACGACACACACCAATCACCAGTCATGCACGAACTCTACCAG 405
Db      1445  CCCACCCGGTGCATTTGTAGGACTCCACACAGTCACCGGTTTGGCATGTACCCCTACCAG 1386
Qy      406  CACCATCGAAGTTACATCCAGTAGGACCCCATATACCTGCCATCGTAGTCCCTAGCGG 465
Db      1385  CAGCATTAAGATTACAATTTGTAGACCCCATATACGTGCCATTTTAGTACCTCGTGGCG 1326
Qy      466  CATCAATGACCCACATTTTGGCCCGGATCGAAACGTCGG-CACCCGCTTTCCGGGTCGATG 524
Db      1325  CATTGATCACCCAAAGTTTGGCTCGATCGAGGCGTCGGCCACCGCCTATGGGGTCCAGC 1266
Qy      525  CGGCCCAACCATGTATGGACAGTTGTTGGTACTCTCGTAGTGGCAGCATTAAGTGAAG 584
Db      1265  CGGCCCAACCGGTGTACGGGCGATTGTTTCGGACCTCGTAGTTGCGACATAAGTACCAAG 1206
Qy      585  TCACAAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGTGAAA 644
Db      1205  TCACAAAGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTATTCATGTTTGTGACA 1146
Qy      645  TTTATATGTGGACAAATTT-----ATTTGGTACTTTTATATATAG 684
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Db      1085  GAGTATGCGGCTTTTTCGCACATAG-----ACATTATCATATATATATTTTAACTTT 1030
Qy      745  GACTAATTTATAACGAAATATATTACAATATGATTTGGTAAACGTTGAGTGGAAAAATG 804
Db      1029  GACTA---GTAATGGAATAATCTCAAGGATGCTTTTGTAAAGTGGAGCGGCTAAAG 973
Qy      805  TATAAGCGCGCTTAAT-ANTTAATTTTATGAATATAGCCTATAGTTACAGTTAAC 863
Db      972  TATAAGCGCGCTTAATAACTATAATTTTATGAATATAG-----AAGTCAA 925
Qy      864  TTTATTTGGTGATAAATTTTGACATATAAACTCTGTACAGTGAC 906
Db      924  TTTATTTGGTGATGCTGCTGACCTATAAGCTCTGTAACGTGAC 882

RESULT 9
NTAP24G/c
LOCUS   NTAP24G N.tabacum ap24 gene. 1549 bp DNA linear PLN 05-MAY-1995
DEFINITION N.tabacum ap24 gene.
ACCESSION X65701
VERSION X65701.1 GI:19782
KEYWORDS osmotin.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1
REFERENCE
AUTHORS Melchers,L.S., Sela-Buurlage,M.B., Vloemans,S.A., Woloshuk,C.P.,
Van Roekel,J.S., Pen,J., van den Elzen,P.J. and Cornelissen,B.J.
TITLE Extracellular targeting of the vacuolar tobacco proteins AP24,
chitinase and beta-1,3-glucanase in transgenic plants
JOURNAL Plant Mol. Biol. 21 (4), 583-593 (1993)
MEDLINE 93192519
PUBMED 8448358
REFERENCE
AUTHORS 2 (bases 1 to 1549)
Melchers,L.S.
TITLE Direct Submission

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Qy	406	CACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTGCCCTAGCGC	465
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Qy	466	CATCAATGACCCACATTTGGCCCCGATCGAAAGCTGG-CACCGCTTTTCGGGGTGCATG	524
Db	607	CATTGATCACCCCAAGTTTGGCCCTCGATCGAGAGCGCCGCCACCGCTTATGGGTGTCGACG	548
Qy	525	CGCGCCAAACGATGTATGGAAGTTGTCGTACCTCGATAGTGGCAGCATAAGTGAAG	584
Db	547	CGCGCCAAACGGTGTACGGACAGTTGTTTCGGACCTCGATAGTGGCAGCATAAGTATAAG	488
Qy	585	TCACAAAGCAAGAAGGAGCAACAAACAAAGATCTCAAGTAGTACCCATCTTGTTCGAA	644
Db	487	TCACCAAGGACGAGAGAGAGAAACAAAGAGATCTCAAGTTGCCCATGTTGTTGGACA	428
Qy	645	TTTATATGTCGACAAATTTATTTTGGTACT-----TTATATATATAGG	685
Db	427	TTTTTTTTTAAACAAGTTGGGTTGTTGGATATAGTGACAAATTTGTTTAGTGGTTTATATAGG	366
Qy	686	GATATGCGGCTTTTGGCACTACGGATTAATAATCGTATATATATAGCAATATCATACTTTG	745
Db	367	GGAAATGCGGCTTTTCTACTATGGATTAATATC-----ATAAATATTTTATTAACATTTG	313
Qy	746	ACTAATTTATAACCGAAATATATTACATATGATTTGGTAAACGTTGAGGTGG-AAAAATG	804
Db	312	ACTA--ATAACCGATATATCTCAAGGATGCTTTGCAAGATGGAGCGGCGCTTTAAA	256
Qy	805	TATAAGAGCGCCTAATATTAATTAATTTTATCAATATAGCCTATAGTTACAAGTTAACT	864
Db	255	CATAAGAGCGCCTAATTAATTAATTTTATCAATATAGCCTATAGTTACAAGTTAACT	864
Qy	865	TTATTTGGTGATTAACCTTTTGACATATAAATCTCTGAACGTGAC	906
Db	207	TTATTTGGTAAATAACGTGACCTATAATCTCTGAACGTGAC	166
RESULT 10			
AR037158/c			
LOCUS			
DEFINITION			
ACCESSION			
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KEYWORDS			
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AUTHORS			
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JOURNAL			
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Best Local Similarity			
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76.9%; Pred. No. 2e-85;			
Conservative 0; Mismatches 163; Indels 41; Gaps 6;			
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Qy	106	AATATTGTTGTCCTCAAAATGGTACAAGGATTTTACATCTCTCGGGTACTTTAAGTT	165
Db	2562	AATATTGTTGTCCTCGAATGTAGTACAGGGTTATTACATCTCTCGGAACCTTAGTT	2503
Qy	166	GACAGGCGATTACCAATTTATTTGCCGTGCATGTAATTTGTGGCATTTCCCTCCAC	225
Db	2502	CGCGGGGACATTCGCGGTTTATATTAGCCGTACAATGAATTTGCATGGCATTTCCCTCCAC	2443

Qy	226	TTGATTAGTCGGGGGAAAGTATCAGGTATATTAATCATCACTAAAGAAATGTCCC	285
Db	2442	TAGGGTTAGTCGGGGGAAAGTATCAGGTATATTAATCATCACTAAAGAAATGTCCC	2383
Qy	286	AGAAATCTAAGTTGTTGAACTGGTCCAAAGCGTACTCGGTAGGGTGTGGTGGTTTC	345
Db	2382	AGAAATCTAAGTTGTTGAACTGGTCCAAAGCGTATTCAGCAAGGTGTGGTGGTTTC	2323
Qy	346	CCCAACCGGTGCACTGCAGGACACCAACCAATCACCAGTCATGCAAGAACCTCTACCAAG	405
Db	2322	CCCAACCGGTGCACTGCAGGACACCAACCAATCACCAGTCATGCAAGAACCTCTACCAAG	2263
Qy	406	CACATCGAAGTTACATCCAGTACGACCCCATATACCTGCATCGTAGTGCCTTAGGGG	465
Db	2262	CAGCATGGAAGTTACATCCAGTACGACCCCATATACCTGCATCGTAGTGCCTTAGGGG	2203
Qy	466	CATCAATGACCCACATTTGGCCCGATCGAAAGTCTGG-CACCCGGTTTCGGGGTCGATG	524
Db	2202	CATTCATGACCCACATTTGGCCCGATCGAAAGTCTGG-CACCCGGTTTCGGGGTCGATG	2143
Qy	525	CGGCCCAACGATGTATGACAGTTGTGGTGTACCTCGATAGTGGGACGATAGTGAAG	584
Db	2142	CGGCCCAACGATGTATGACAGTTGTGGTGTACCTCGATAGTGGGACGATAGTGAAG	2083
Qy	585	TCACAAAGCAAGGAGGAGAAACAAAGATCTCAAGTAGCCCATGTTTGTGAAA	644
Db	2082	TCACAAAGCAAGGAGGAGAAACAAAGATCTCAAGTAGCCCATGTTTGTGAAA	2023
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Qy	686	GATATGGCGGTTTGGCAGTACCGATATTAATCGTATTATATAGCAATATCATCTTTG	745
Db	1908	GGAATGGCGGTTTTCGTACTATGATTAATTAATTTTATGAATATAG-----AAGTCAAT	1803
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Db	1907	ACTA--ATAACGATATATCTCAAGATGCTTTGGCAAAGATGGAGGGCGGCTTAAA	1851
Qy	805	TATAGAGCGCCTAATAATTAATTTATGAATATAGCCTATAGTTACAGTTAACT	864
Db	1850	CATAAGAGCGCCTAATAATTAATTTATGAATATAG-----AAGTCAAT	1803
Qy	865	TTATTTGGTATACCTTTGACATATAAATCTCTGTAACGTGAC	906
Db	1802	TTATTTGGTATACCTTTGACATATAAATCTCTGTAACGTGAC	1761
RESULT 11			
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LOCUS			
DEFINITION			
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Genomic, 3033 nt].			
ACCESSION			
S40046			
VERSION			
S40046.1			
KEYWORDS			
SOURCE			
ORGANISM			
Nicotiana tabacum (common tobacco)			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
asterids; lamiales; Solanales; Solanaceae; Nicotiana.			
1 (bases 1 to 3033)			
REFERENCE			
AUTHORS			
Nelson, D.E., Raghothama, K.G., Singh, N.K., Hasegawa, P.M. and			
Bressan, R.A.			
TITLE			
Analysis of structure and transcriptional activation of an osmotin			
gene			
JOURNAL			
Plant Mol. Biol. 19 (4), 577-588 (1992)			
MEDLINE			
92329718			
PUBMED			
1385735			
REMARK			
GenBank staff at the National Library of Medicine created this			
entry [NCBI Gibbs 108425] from the original journal article.			
This sequence comes from Fig. 1A.			

FEATURES		Location/Qualifiers	
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ORIGIN		Query Match	
		Best Local Similarity 30.0%; Score 479.2; DB 8; Length 3033;	
		Matches 678; Conservative 0; Mismatches 163; Indels 41; Gaps 6;	
Qy	46	GGTATCTTTGTTTGAAGAAATTTGGAAGAACGTAGGACACATGGACCTGGGTGCAAC	105
Db	2622	GGCATCTTTGTTTGAAGAAATTTGGAAGAAATTTGGAAGAACGTAGGACACATGGGTGCAAC	2563
Qy	106	AATATTGTTGCTCCAAATGTGTAAGGATTTTACATCTCCCGGGTACTTTAAAGTT	165
Db	2562	AATATTGTTGCTCCCGAATGTAGTACAGGGTTATTACATCTCCCGGAACTTAAAGTT	2503
Qy	166	GACCAAGGCATTCACATTTATTTGCGGTGCAATTTGAATTTGTTGGATTCCTCCAC	225
Db	2502	CGCGGGACATTCGCGGTTTATATTAGCCGTACAAATGAATTTGATGTCATTTCCCTCCAC	2443
Qy	226	TTGGATTAGTCGGGGGAAAGTATCAGGTATTAATTAATTAATTAATTAATTAATTAAT	285
Db	2442	TAGGTTAGTCGGGGGAAAGTATCAGGTATTAATTAATTAATTAATTAATTAATTAAT	2393
Qy	286	AGAAATCTAAGTTGTTGAACTGGTCCAAAGCGTACTCGGTAGGGTGTGGTGGTTTC	345
Db	2382	AGAAATCTAAGTTGTTGAACTGGTCCAAAGCGTATTCAGCAAGGTGTGGTGGTTTC	2323
Qy	346	CCCAACCGGTGCACTGCAGGACACCAACCAATCACCAGTCATGCAAGAACCTCTACCAAG	405
Db	2322	CCCAACCGGTGCACTGCAGGACACCAACCAATCACCAGTCATGCAAGAACCTCTACCAAG	2263
Qy	406	CACATCGAAGTTACATCCAGTACGACCCCATATACCTGCATCGTAGTGCCTTAGGGG	465
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Qy	466	CATCAATGACCCACATTTGGCCCGATCGAAAGTCTGG-CACCCGGTTTCGGGGTCGATG	524
Db	2202	CATTGATCACCACAAAGTTTGGCTCGATCGAGACCCCGCCCATGCGGTGTGCGACG	2143
Qy	525	CGGCCCAACGATGTATGACAGTTGTGGTGTACCTCGATAGTGGGACGATAGTGAAG	584
Db	2142	CGGCCCAACGATGTATGACAGTTGTGGTGTACCTCGATAGTGGGACGATAGTGAAG	2083
Qy	585	TCACAAAGCAAGGAGGAGAAACAAAGATCTCAAGTAGCCCATGTTTGTGAAA	644
Db	2082	TCACCAAGCAAGGAGGAGAAACAAAGATCTCAAGTAGCCCATGTTTGTGAAA	2023
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Db	2022	TTTTTTTAAACAGTTGGTGTGGTATAGTGAAGATTTTGTGACTTTTATATAGG	1963
Qy	686	GATATGGCGGTTTGGCAGTACCGATATTAATCGTATTATATAGCAATATCATCTTTG	745


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Db      1962  GGAATGCGGCTTTTCGTACTATGATATTAATC-----ATAAATATTATTAACTTTG 1908
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Db      1907  ACTA--ATAACGGATATATCTCAAGGATGCTTTGGCAAAGATGGAGCGGCTTTAAA 1851
Qy      805   TATAAGAGCCGCTTAATAATTATTATTATGATATAGCTTATAGCTTAACTTAACT 864
Db      1850  CATAAGAGCCGCTTAATAATTATTATTATGATATAG-----AAGTCAAT 1803
Qy      865   TTATTGGTGATACTTTGACATATAAACTCTGAACGTGAC 906
Db      1802  TTATTGGTATAACGTGACCTATAATCTCTGAACGTGAC 1761

RESULT 12
AY007309/c      818 bp      mRNA      linear      PLN 22-JAN-2001
LOCUS          Solanum dulcamara cryoprotective osmotin-like protein mRNA,
DEFINITION     complete cds.
ACCESSION      AY007309
VERSION        AY007309.1  GI:10445202
KEYWORDS
SOURCE
ORGANISM       Solanum dulcamara
                Solanum dulcamara
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE      1 (bases 1 to 818)
                Newton,S.S. and Duman,J.G.
                An osmotin-like cryoprotective protein from the bittersweet
                nightshade Solanum dulcamara
                Plant Mol. Biol. 44 (5), 581-589 (2000)
JOURNAL
MEDLINE        21039368
PUBMED         11198420
REFERENCE      2 (bases 1 to 818)
                Newton,S.S. and Duman,J.G.
                Direct Submission
                Submitted (23-AUG-2000) Biological Sciences, University of Notre
                Dame, Galvin Life Sciences Bldg., Notre Dame, IN 46556, USA
JOURNAL
FEATURES       source
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                29.1%; Score 463.6; DB 8; Length 818;
                Query Match
                Best Local Similarity 87.2%; Pred. No. 2.7e-82;
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Qy      46   GGTATCTTTGTTGAAAAAATTGAAAAAGACGTAGGACCATGGACCTTGGGTGCAAC 105
Db      610  GGATCTTTGTTGAAAAAATCTCGAACAGTCAGTAGGATTACATGGACCTTGGGTGCAAC 551
Qy      106  AATATGTTGCTCCCAATGGTGTACAGGATTTGTATCATCTCCCGGTACTTTAAGTT 165
Db      550  AATATGTTGCTCCCAACGTGGTACAGGTTGTTTACATCTCCCGGCACTCTAAGTG 491
Qy      166  GACCAAGGCATTACCACTTATTTGCGTGCAATGAATTTGTGGCAATTCCTCCAC 225
Db      490  AACCAGGACATTCACCATTTATGTTAGCGTGCAATGAATTCATGTCATTTCTCTCAC 431

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Qy      226  TTGGATTAGTCGGGGGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCC 285
Db      430  TAGGATTGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCGACTAAAGAAATGTCCC 371
Qy      286  AGAAATCTAAGTTGTTGAACCTCGTCCAAAGCGCTACTCGGCTAGGGTGTGTTGGTGTTCG 345
Db      370  AGAAATCTAAGTTGTTGAACCTCGTCCAAAGCGCTACTCGGCTAGGGTGTGTTGGGTTTGC 311
Qy      346  CCCACCCGGTGCACTGTCAGGACACACCAACATACCACTGATGACAGCACTTACCAAG 405
Db      310  CCCACCCGATACACTGTAGTACCCACCAATACCACTGATGACAGCACTTACCAAG 251
Qy      406  CACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCGCATCTAGTGCCTTAGGGG 465
Db      250  CACCATTTGAAGTTACAACCGATGACCCCATATAGTGCCTTCTAGTGCCTTGGTGGT 191
Qy      466  CATCAATGACCCACATTTTGGCCCGGATCGAAACGTCG-GCACCCTGTTTCGGGGTGCATG 524
Db      190  CATTGATGACCCATGTTTGGCTCGATCTAGACGTCGACCCACCTATCGGGGTGCGACG 131
Qy      525  CGCCCAACAGATGATGACAGATGTTTGGCTGACCTCGATGTCGATGTCGACGATAGTGAAG 584
Db      130  CGCCCAACAGCTGTACGGACAGTGTGTTTCGGACCTCGATGTCGACGATAGTGAAGTATAAG 71
Qy      585  TCACAAAACCAAGAGGGAGAAAACAAAAGAAAGATCTCAAG---TAGCCCATGTTTGTG 641
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Qy      642  AAATTATAT 651
Db      10  AACTATTTT 1

RESULT 13
AF473702/c      729 bp      DNA      linear      PLN 25-FEB-2002
LOCUS          Solanum nigrum osmotin-like protein gene, complete cds.
DEFINITION     AF473702
ACCESSION      AF473702
VERSION        AF473702.1  GI:18874518
KEYWORDS
SOURCE         Solanum nigrum (black nightshade)
ORGANISM       Solanum nigrum
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE      1 (bases 1 to 729)
                Jami,S.K. and Kirti,P.B.
                PCR-based cloning of an osmotin-like protein gene from Solanum
                nigrum
                Unpublished
                2 (bases 1 to 729)
                Jami,S.K. and Kirti,P.B.
                Direct Submission
                Submitted (21-JAN-2002) Department of Plant Sciences, University of
                Hyderabad, Gachibowli, Hyderabad, A.P 500046, India
JOURNAL
FEATURES       source
                location/Qualifiers
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Query Match      29.1%; Score 463.4; DB 8; Length 729;
Best Local Similarity 87.8%; Pred. No. 2.9e-82;
Matches 517; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 46 GGTATCTTTGTTGAAAGAAATGGAAGACAGTAGGACACACATGGACCTTGGGTGCAAC 105
DB 589 GGCATCTTTGTTGAAAGAAATTTGACAAATCCCGTAGGACACACATGGACCTTGGGTGCAAC 530

QY 106 AATATTGTTGTCCTCCAAATGTTGTAAGGATTTACATCTCTCCGGGTACTTTAAGTT 165
DB 529 AATATTGTTGTCCTCCGAAAGTGTGTAAGGATTTGTAAGGATTTACATCTCTCCGGGTACTTTAAGTT 470

QY 166 GACAGGGCATTACCAATTTATATTGCGGTGCAATGGAATGTTGTCATTTCCCTCCAC 225
DB 469 CAGCAGGACATTCCACATTTATATTGCGGTGCAATTTGAATTTGATGACATTTCCCTCCAC 410

QY 226 TTGATTAGTCGGGGCGAAGTGTATCGGTATATTAAATCCATCAATCAAGAAATGTCCTC 285
DB 409 TAGGATTGTTGCGGGCGAAGTGTATCGGTATATTAAATCCATCAATCAAGAAATGTCCTC 350

QY 286 AGAAATCTAAGTTGTTGAACTGTTCCAAAGGCTACTCGGTAGGGTGTGTTGGTGTTC 345
DB 349 AGAAATCTAAGTTGTTGAACTGTTCCAAAGGCTACTCGGTAGGGTGTGTTGGGTTTC 290

QY 346 CCCACCGGTGCTACGAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAAT 405
DB 289 CCCACCGGTGCTACGAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAAT 230

QY 406 CACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCTAGTGTGCTGCTAGGCG 465
DB 229 CACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCTAGTGTGCTGCTAGGCG 170

QY 466 CATCAATGACCCCATTTGCGGCGGATCGAAAGCTGCG- GCACCGGCTTTGCGGGTGCATG 524
DB 169 CATGATGACCCCATTTGCGGCGGATCGAGAGCTGCGACCGCTATCGGGGTGCGAG 110

QY 525 CCGCCCAAGGATGATGAGCAGTTGTTGCGTACCTCGATGAGTGGCAGCATAGTGAAG 584
DB 109 CCGCCCAAGGATGATGAGCAGTTGTTGCGTACCTCGATGAGTGGCAGCATAGTGAAG 50

QY 585 TCACAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCAT 633
DB 49 TCACAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCAT 1

RESULT 14
LOCUS AY093595 917 bp mRNA linear PLN 17-OCT-2002
DEFINITION Lycopersicon esculentum PR-5x (PR-5) mRNA, complete cds.
ACCESSION AY093595
VERSION AY093595.1 GI:20750096
KEYWORDS
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 917)
Rep.M., Dekker.H.L., Vossen.J.H., De Boer.A.D., Houterman.P.M.,
Speijer.D., Back.J.W., De Koster.C.G. and Cornelissen.B.J.C. in
Mass Spectrometric Identification of Isoforms of PR Proteins in
Xylem Sap of Fungus-Infected Tomato
Plant Physiol. 130 (2), 904-917 (2002)
22264016
PUBMED 12376655
REFERENCE 2 (bases 1 to 917)
Rep.M., Dekker.H.L., Vossen.J.H., de Boer.A., Houterman.P.,
Speijer.D., Back.J.W. and Cornelissen.B.J.C.
Direct Submission
Submitted (28-MAR-2002) Plant Pathology, University of Amsterdam,
Kruislaan 318, Amsterdam 1098SM, Netherlands
Location/Qualifiers
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Best Local Similarity 86.2%; Pred. No. 3.2e-82;
Matches 524; Conservative 0; Mismatches 83; Indels 1; Gaps 1;

QY 46 GGTATCTTTGTTGAAAGAAATTTGAAAGACAGTAGGACACACATGGACCTTGGGTGCAAC 105
DB 608 GGCATCTTTGTTGAAAGAAATCTCGAAATTTTGTAGGACACACATGGGCTTTAGTACAC 549

QY 106 AATATTGTTGTCCTCCAAATGTTGTAAGGATTTACATCTCTCCGGGTACTTTAAGTT 165
DB 548 AATATTGTTGTCCTCCGAAACGTCGTACAAAGGTTGTTACATCTCTCCGGGTACCTAAGT 489

QY 166 GACAGGGCATTACCAATTTATATTGCGGTGCAATGGAATGTTGTCATTTCCCTCCAC 225
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QY 226 TTGATTAGTCGGGGCGAAGTGTATCGGTATATTAAATCCATCAATCAAGAAATGTCCTC 285
DB 428 TAGGATTGTTGGGCGAAGTGTATCGGTATATTAAATCCGTCACCAAGAAATGTCCTC 369

QY 286 AGAAATCTAAGTTGTTGAACTGTTCCAAAGGCTACTCGGTAGGGTGTGTTGGTGTTC 345
DB 368 AGAAATCTAAGTTGTTGAACTGTTCCAAAGGCTACTCGGTAGGGTGTGTTGGGTTTC 309

QY 346 CCCACCGGTGCTACGAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAAT 405
DB 308 CCCACCGGTGCTACGAGGACACCAATCAATCAATCAATCAATCAATCAATCAATCAAT 249

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DB 248 CACCATGAAATTTGCAATTTAGTACGACCCCATATACCTGCTAGTGTGCTGCTAGGCG 189

QY 466 CATCAATGACCCCATTTGCGGCGGATCGAAAGCTGCG- GCACCGGCTTTGCGGGTGCATG 524
DB 188 CATGATGACCCATTTGCGGCTGCTGAGAGCTGCGACCGCTATCGGGGTGCATG 129

QY 525 CCGCCCAAGGATGATGAGCAGTTGTTGCGTACCTCGATGAGTGGCAGCATAGTGAAG 584
DB 128 CTGCCCCAAACGGTGTAGGACAAATTTGTCGTACCTCGATGAGTGGCAGCATAGTGAAG 69

QY 585 TCACAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCATTTTGTGAAA 644
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QY 645 TTTATATG 652
DB 8 TATTTTG 1

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RESULT 15
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LOCUS       744 bp DNA linear PLN 12-MAR-2002
DEFINITION Solanum nigrum osmotin-like protein precursor (OLP) gene, complete
            cds.
ACCESSION  AF450276
VERSION     AF450276.1 GI:19401630
SOURCE     Solanum nigrum (black nightshade)
ORGANISM   Solanum nigrum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE  1 (bases 1 to 744)
AUTHORS   Campos,M.A., Ribeiro,S.G., Rigden,D.J., Monte,D.C. and Grossi de
            Sa,M.F.
TITLE     Pathogenesis related-like genes of Solanum nigrum: cloning and
            characterization of genes coding for neutral and basic PR5-like
            proteins
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 744)
AUTHORS   Campos,M.A., Ribeiro,S.G., Monte,D.C. and Grossi de Sa,M.F.
TITLE     Direct Submission
JOURNAL    Submitted (21-NOV-2001) PBI, Embrapa Genetic Resources and
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ORIGIN

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Query Match      29.0%; Score 463; DB 8; Length 744;
Best Local Similarity 87.6%; Pred. No. 3.5e-82;
Matches 516; Conservative 1; Mismatches 71; Indels 1; Gaps 1;

Qy  46  GGTATCTTTGTTGAAAAAATTTGAAAAAGACGTAGACACACATGGACCTTGGGTGCAAC 105
Db  589  GGCATCTTTGTTGAAAAAATTTGACAAATTCGCTAGGACCACATGGACCTTGGGTGCAAC 530
Qy  106  AATATTGTTGTCCTCCAAATGTTGTACAAAGATTGTTACATCCTCCGGGTACTTTAAGTT 165
Db  529  AATATTGTTGTCCTCCAAATGTTGTACAAAGATTGTTACATCCTCCGGGTACTTTAAGTT 470
Qy  166  GACCAGGCATTCACCAATTATATTTCGCTGCAATGAATTGTTGGCATTCCCTCCAC 225
Db  469  CAGCAGGACATTCACCAATTATATTTCGCTGCAATGAATTGTTGGCATTCCCTCCAC 410
Qy  226  TTGGATTAGTCGGGGGAAAGTCATCGGTATTTAAATCCATCACTAAAGAAATGTCOC 285
Db  409  TAGGATTGTCGGGGGAAAGTCATCGGTATTTAAATCCATCACTAAAGAAATGTCOC 350
Qy  286  AGAAATCTAAGTTTGTGAACCTGGTCCAGGCGTACTCGGCTAGGGTGTGTTGGTTTGC 345

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Job time : 6048.75 secs

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Db  349  AGAAATCTAGATTGCTGAACCTGGTTCAAAGCGGTATTCGGCTAGGTGTTTGGGGTTTGC 290
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Db  289  CCCACCCGGTGCACTGCGAGGACCCCAACAATCAACCGGTCTGGCATGAACCTCTACCAG 230
Qy  406  CACCATCGAAGTTACATCCAGTACGACCCCAATATACCTGCCATCGTAGTGCCTTAGGCG 465
Db  229  CACCATCGAAGTTGCAATTAGTACGACCCCAATATTCGTGCCATACTAGTGCCTTTGGTG 170
Qy  466  CATCAATGACCCACATTTTGGCCCCCGATCGAAACGTG-GCACCCCGCTTTTCGGGGTTCGATG 524
Db  169  CATTGATGACCCATGCTCTGGCCTCGATCGAGACGTGCGACCAACCGCTATCGGGGTCGACG 110
Qy  525  CGGCCCCAACGATGATGGACAGTTGTTGCGTACCTCGATAGTGGCAGCATAAAGTGAAG 584
Db  109  CGGCCCCAACGCTGATGGACAGTTGTTTCGGACCTCGAAAGAGGTAGCATAAAGTATAAG 50
Qy  585  TCACAAAACGAAGAGGAGGAGAAAACAAAAGAAAGATCTCAAGTAGCCCAT 633
Db  49  TCACAAAAGTAGGAGGAGGAGAAAACAAAAGAAAGATCTCGAGTAGCCCAT 1

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 03:32:09 ; Search time 570.148 Seconds
(without alignments)
11884.422 Million cell updates/sec

Title: US-10-051-307-1
Perfect score: 1595
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373663 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: Geneseq2001as:*
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6: Geneseq2002s:*
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8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1593.4	99.9	1595	6	Abk90560 Potato pr
2	1483.8	93.0	1598	6	Abk90561 Potato pr
3	1375.2	86.2	1546	6	Abk90562 Potato pr
4	479.2	30.0	3033	2	Aav52754 Nicotiana
5	479.2	30.0	3033	2	Aax16340 Tobacco o
6	430.2	27.0	883	2	Aaq15269 Osmotin-1
7	430.2	27.0	884	2	Aaq15270 Emocodes C
8	428.2	26.8	741	2	Aav68641 Nucleotid
9	362.2	22.7	1004	2	Aaq21414 Encodes o
10	197.8	12.4	906	3	Aac47993 Arabidops
11	186.2	12.3	902	3	Aac47227 Arabidops
12	195.6	12.3	735	6	Abz14313 Arabidops
13	195.6	12.3	735	7	Abz42096 Arabidops
14	195.6	12.3	735	7	Ada68525 Arabidops
15	195.6	12.3	950	6	Abn98566 Arabidops
16	170.4	10.7	875	5	Aac84839 Sunflower
17	166.8	10.5	771	3	Aaz29511 Asparagus
18	155.2	9.7	900	1	Aan90842 Fragment
19	155.2	9.7	900	2	Aav62808 Tobacco P
20	155.2	9.7	900	2	Aav72992 PR-R major
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23	128.6	8.1	500	3	Aaa40422 Potato in

ALIGNMENTS

RESULT 1
ABK90560
ID ABK90560 standard; DNA; 1595 BP.

XX
AC ABK90560;

XX
DT 15-NOV-2002 (first entry)

XX
DE Potato proteinase inhibitor 1 (pinl) gene promoter isoform 1.

XX
KW Potato; proteinase inhibitor 1; pinl; promoter; ds; plant;

XX
KW Controlled Environmental Agriculture; crop cultivation.

XX
OS Solanum tuberosum.

XX
PN WC200259333-A2.

XX
PD 01-AUG-2002.

XX
PF 18-JAN-2002; 2002WO-US001287.

XX
PR 23-JAN-2001; 2001US-0263224P.

XX
PA (DAIZ/) DAI Z.

XX
PA (SHIL/) SHI L.

XX
PA (HOOK/) HOOKER B S.

XX
PI Dai Z, Shi L, Hooker BS;

XX
DR WPI; 2002-608457/65.

XX
PT New proteinase inhibitor 1 (pinl) or aminotransferase (amt) gene promoter isoforms derived from potato, useful in manipulating expression of genes and in Controlled Environmental Agriculture for heterologous protein production.

XX
PS Claim 2; Fig 1; 43pp; English.

XX
CC The invention relates to polynucleotides having proteinase inhibitor 1 (pinl) or aminotransferase (amt) gene promoter activity. Isoforms of pinl and amt gene promoters are useful in manipulating expression of genes, particularly in transformed plant cells. The gene promoters are useful in constructing gene expression vectors and in Controlled Environmental Agriculture for heterologous protein production. The vectors are useful in facilitating the expression and/or secretion of heterologous proteins in cell culture or by crop cultivation. The new gene promoter isoforms

Ada71704 Rice gene
Aa58991 Diospyros
Aa58992 Diospyros
Aa58993 Diospyros
Aa61184 PR-R major
Aa40215 Gene enco
Ab85936 Arabidops
Aa91491 Zeamatin
Aa28688 Ripening
Ada4913 PING152CV
Ada71064 Rice gene
Aa40914 PING323CV
Aa71063 Rice gene
Aa70934 DNA seque
Abq78707 Nucleotid
Abq78703 Nucleotid
Aa59196 Modified
Aa59192 Thaumatin
Aa70933 DNA seque
Aa50328 Sequence
Ada6930 Rice gene
Aa06312 Thaumatin
Aa20003 Preprotha

8.0 2000 7 ADA71704
7.4 693 2 Aa58991
7.4 627 2 Aa58992
7.2 950 1 Aa61184
6.8 705 1 Aa40215
6.7 343 6 Ab85936
6.7 894 2 Aa91491
6.7 808 2 Aa28688
6.1 1309 2 Aa40913
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5.0 961 1 Aa20003

C 24 127
C 25 118.4
C 26 117.4
C 27 115.6
C 28 107.8
C 29 106.8
C 30 106.4
C 31 106.2
C 32 97.4
C 33 96.8
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C 35 94.2
C 36 90.6
C 37 90.6
C 38 90.6
C 39 90.6
C 40 90.6
C 41 89
C 42 89
C 43 88.8
C 44 84.6
C 45 80

CC provide high level, stable and controllable expression that is
CC temporarily, environmentally, or developmentally regulatable. This
CC sequence represents a potato pin1 gene promoter isoform

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DB	1	GTAAATACGACTC	ACTATATAGGCGACGCGTGGTCGACGGCCCTGGCTGGTATCTTTGTTTGA	60		
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DB	61	AAAAATGGAAAAGAA	CGTAGGACCTTGGGTGCGAACAAATATTGTTGTCCTC	120		
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DB	121	CAAAATGGTGTACA	AGGATGTTTACATCTCCGGGTACTTTAAAGTTGACACAGGGCATTCAC	180		
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QY	421	ATCCAGTAGACCC	CCATATATCTGCGATCGTAGTGCCCTTAGCGCATCAATGACCCACA	480		
DB	421	ATCCAGTAGACCC	CCATATATCTGCGATCGTAGTGCCCTTAGCGCATCAATGACCCACA	480		
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DB	481	TTTGGCCCCGATCG	AAACGTCGGCACCCGCTTTCGGGGTCGATGCGCGCCAAACAGATGTA	540		
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DB	541	TGGACAGTTGTTG	CGTACTCGATAGTGGCAGCATAAAGTGAAGTCAAAAAAGCAAGAG	600		
QY	601	GGAGAAAAACAAG	AAAGATCTCAAGTAGCCCATGTTTGGTAATTTATATGTGACACAA	660		
DB	601	GGAGAAAAACAAG	AAAGATCTCAAGTAGCCCATGTTTGGTAATTTATATGTGACACAA	660		
QY	661	TTATTTTGGTACT	TTATATATAGGATATGGGGCTTTTGGCATACCGATATTAATCG	720		
DB	661	TTATTTTGGTACT	TTATATATAGGATATGGGGCTTTTGGCATACCGATATTAATCG	720		
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DB	781	GGTAAACGTTGAG	TGGGAAAAATGTATAAGAGCGCGCTTAATAATTTATTTATGAAT	840		
QY	841	ATAGCCTATAGTT	ACAAGTTAACTTTATTTGGTGTATAACTTTTCACATATAAACTCTGTAA	900		
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QY	901	CGTGA	CGGAATTTTTCTTTAAACACTAAATATTAAAAAGCAGCTATTTTCAGATTTTTCGTG	960		
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ID	ABK90561 standard; DNA; 1598 BP.
XX	
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XX	ABK90561;
XX	AC
XX	15-NOV-2002 (first entry)
DT	
XX	
DE	Potato proteinase inhibitor 1 (pin1) gene promoter isoform II.
XX	
KW	Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
XX	Controlled Environmental Agriculture; crop cultivation.
XX	
OS	Solanum tuberosum.
XX	
PN	WO200259333-A2.
XX	
PD	01-AUG-2002.
XX	
PF	18-JAN-2002; 2002WO-US001287.
XX	
PR	23-JAN-2001; 2001US-0263224P.
XX	
PA	(DAIZ/) DAI Z.
PA	(SHIL/) SHI L.
PA	(HOOK/) HOOKER B S.
XX	

PI Dai 2, Shi L, Hooker BS;
XX WPI; 2002-608457/65.
XX New proteinase inhibitor 1 (pini) or aminotransferase (amt) gene promoter
PT isoforms derived from potato, useful in manipulating expression of genes
PT and in Controlled Environmental Agriculture for heterologous protein
PT production.
XX Claim 2; Fig 2; 43pp; English.
XX The invention relates to polynucleotides having proteinase inhibitor 1
CC (pini) or aminotransferase (amt) gene promoter activity. Isoforms of pini
CC and amt gene promoters are useful in manipulating expression of genes
CC particularly in transformed plant cells. The gene promoters are useful in
CC constructing gene expression vectors and in Controlled Environmental
CC Agriculture for heterologous protein production. The vectors are useful
CC in facilitating the expression and/or secretion of heterologous proteins
CC in cell culture or by crop cultivation. The new gene promoter isoforms
CC provide high level, stable and controllable expression that is
CC temporarily, environmentally, or developmentally regulatable. This
CC sequence represents a potato pini gene promoter isoform
XX
SQ Sequence 1598 BP; 507 A; 299 C; 300 G; 492 T; 0 U; 0 Other;
Query Match 93.0%; Score 1483.8; DB 6; Length 1598;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 47; Indels 5; Gaps 3;
QY 1 GTAATAGACTCACTAPAGGCGACGGTGTGCGACGGCCCTGCTGGTATCTTTGTTGA 60
DB 1 GTAATAGACTCACTAPAGGCGACGGTGTGCGACGGCCCGGGCTGGTATCTTTGTTGA 60
QY 61 AAAAAATGGAAAGAAAGCTAGGACCAATGACATGACCTTGGGTGCAACATATTTGTCCTC 120
DB 61 AAAAAATGGAAAGAAAGCTAGGACCAATGACATGACCTTGGGTGCAACATATTTGTCCTC 120
QY 121 CAAATGGTACAAAGGATTTGTACATCTCGGTACTTTAAGTTGACCAAGGCAATTCAC 180
DB 121 CAAATGGTACAAAGGATTTGTACATCTCGGTACTTTAAGTTGACCAAGGCAATTCAC 180
QY 181 CATTATATTTGCGGTGCAATGATTTGGGCAATTTCCCTCCATTTGGATTAGTGGGG 240
DB 181 CATTATATTTGCGGTGCAATGATTTGGGCAATTTCCCTCCATTTGGATTAGTGGGG 240
QY 241 CGAAGTCATCGGTATATTAATCCATCACTAAGAAATGTCACAGAAATCTAAGTTGT 300
DB 241 CGAAGTCATCGGTATATTAATCCATCACTAAGAAATGTCACAGAAATCTAAGTTGT 300
QY 301 TGAATCGTCCAAAGCGTACTCGGCTAGGCTGTTTGGTGGTTTCCCGCCACCGGTGCACT 360
DB 301 TGAATCGTCCAAAGCGTACTCGGCTAGGCTGTTTGGTGGTTTCCCGCCACCGGTGCACT 360
QY 361 GCAGACACCAACCAATCAGTCATGACGAACTCTACAGCACTTACAGCACTCGAAGTTAC 420
DB 361 GCAGACACCAACCAATCAGTCATGACGAACTCTACAGCACTTACAGCACTCGAAGTTAC 420
QY 421 ATCCAGTACGACCCCATATAGTGCCTAGTGGCTAGTGGCTAGTGGCTAGTGGCTAGT 480
DB 421 ATCCAGTACGACCCCATATAGTGCCTAGTGGCTAGTGGCTAGTGGCTAGTGGCTAGT 480
QY 481 TTTGGCCCGGATCGAAACGTCGCGACCGCTTTCGGGGTCGATCGCGCCCAACGATGTA 540
DB 481 TTTGGCCCTCGATCGAGACGTCGGGACCGCTATCGGGTCGATCGCGCCCAACGATGTA 540
QY 541 TGGCAGTTGTTG - CGTACCTCGATAGTGCAGCATAAGTGAAGTCAAAAAAGCAAGA 598
DB 541 TGGCAGTTGTTGCGCGGTACCTTCGATAGTGCAGCATAAGTGAAGTCAAAAAAGCAAGA 600
QY 599 AGGGAGAAAAAAGAAAGATCTCAAGTAGCCCATGTTTGTGAAATTTATATGTGACA 658
DB 601 AGGGAGAAACCAAAAGAAAGATCTCAAGTAGCCCATGTTTGTGAAATTTATATGTGACA 660

QY 659 AATTATTTTGGTACTTTTATATAGGATATAGCGGCTTTTGGCACTACGGATATTAAT 718
DB 661 AATTATTTTGGTACTTTTATATAGGATATAGCGGCTTTTGGCACTACGGATATTAAT 720
QY 719 CGTATTATATAGCAATATCATACCTTTGACTTAATTAATAAGCAATATATTAATATGAT 778
DB 721 CGTATTATATACCAATATCATACCTTTGACTTAATTAATAAGCAATATATTAATATGAT 780
QY 779 TTGGTAAACGTTGAGGTGGAAAAATGATATAGAGCCGCTAATAATTAATTAATTTATGA 838
DB 781 TTGGTAAACGTTGAGGTGGAAAAATGATATAGAGCCGCTAATAATTAATTAATTTATGA 840
QY 839 ATATAGCCTATAGTTTACAAAGTTAACTTTTATTTGGTGATACTTTGACATATAAACTCTGT 898
DB 841 ATATAGCCTATAGTTTACAAAGTTAACTTTTATTTGGTGATACTTTGACATATAAACTCTGT 900
QY 899 AACGTGACGGAATTTTCTTAAACTAAATTAATAAGCACTATTTTTCAGATTTTCG 958
DB 901 AACGTGACGGAATTTTCTTAAACTAAATTAATAAGCACTATTTTTCAGATTTTCG 960
QY 959 TGGCCAAAAGTTTCTTGCACTACTTATCTATGCCCCATTTTACTTTTATGCTTCTAGCCTTC 1018
DB 961 TGGCCAAAAGTCTCTTGCACTACTTATCTATGCCCCATTTTACTTTTATGCTTCTAGCCTTC 1020
QY 1019 TAGGTACACGTTTGAACATATAAAATCATATAAATTTGAAGTAAATAATTTAGTTTTCCT 1078
DB 1021 TAGGTACACGTTTGAACATATAAAATCATATAAATTTGAAGTAAATAATTTAGTTTTCCT 1080
QY 1079 TTCATATTACTCGTAGGATCATTTTGTAGTCAATCTGAATATACAAACCATTTCTGAT 1138
DB 1081 TTCATATTACTCGTAGGATCATTTTGTAGTCAATCTGAATATACAAACCATTTCTGAT 1140
QY 1139 TTTAAATACCAACCATTTTCC - AAGGGGAAGTCTATGTGATCCGTGACAAAGTGGTTT 1196
DB 1141 TTTAAATACCAACCATTTTCCCTAATGCGGAAGTCTATGTATCGTGGCAAGT - GTTT 1199
QY 1197 GATTATCTTAGTCTAGATTTGGAGTCACAACTTTTGTAGTGCRAATATCTATTAAGAAGACC 1256
DB 1200 GATTATCTTAGTCTAGATTTGGAGTCACAACTTTTGTAGTGCRAATATCTATTAAGAAGACC 1259
QY 1257 CTTATTTGATGCAATATCTTATTAAGAAGACCCTTATTCATGCTTTTATTTTATTTTACGAT 1316
DB 1260 CTTATTTGATGCAATATCTTATTAAGAAGACCCTTATTCATGCTTTTATTTTATTTTACGAT 1319
QY 1317 CGGAGCATGGATATATTTACTAATTAATAAATTTGGAAGAAATTTGATCGAAGCACTC 1376
DB 1320 CGGAGCATGGATATATTTACTAATTAATAAATTTGGAAGAAATTTGATCGAAGCACTC 1379
QY 1377 AAGCTTATCGTCGATCCACATTAATAAATACGTTAGTGGCTGCTTTTGAAGAAACCAAGT 1436
DB 1380 AAGCTTATCGTCGATCCACATTAATAAATACGTTAGTGGCTGCTTTTGAAGAAACCAAGT 1439
QY 1437 GGATCATGTATATTTAGTTTAAATATCTCTATAAATATCTCTATAAATACCTCTATCTATAA 1496
DB 1440 GGATCATGTATATTTAGTTTAAATATCTCTATAAATATCTCTATAAATACCTCTATAA 1499
QY 1497 CTTAAATGCACTCAACACCAATATAAATCTAGATTTCTTTAAAGAAATTTGAGAAATTA 1556
DB 1500 CCAATATACATCTAACACACCAATATAAATCTAGATTTCTTTAAAGAAATTTGAGAAATTA 1559
QY 1557 ATGGAGGCAAAATAGTCTATGTTGGAAGTTGGTTGCTTTC 1595
DB 1560 ATGGAGGCAAAATAGTCTATGTTGGAAGTTGGTTGCTTTC 1598

RESULT 3
ID ABK90562
XX ABK90562 standard; DNA; 1546 BP.
AC ABK90562;
XX
DT 15-NOV-2002 (first entry)
XX

DE Potato proteinase inhibitor 1 (pin1) gene promoter isoform III.

KW Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
Controlled Environmental Agriculture; crop cultivation.

XX Solanum tuberosum.

XX WO200259333-A2.

FN 01-AUG-2002.

XX 18-JAN-2002; 2002WO-US001287.

XX 23-JAN-2001; 2001US-0263224P.

PR (DAIZ/) DAI Z.

PA (SHIL/) SHI L.

PA (HOOK/) HOOKER B S.

XX Dai Z, Shi L, Hooker BS;

XX WPI; 2002-608457/65.

XX New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter

PT isoforms derived from potato, useful in manipulating expression of genes

PT and in Controlled Environmental Agriculture for heterologous protein

PT production.

XX Claim 2; Fig 3; 43pp; English.

XX The invention relates to polynucleotides having proteinase inhibitor 1

XX (pin1) or aminotransferase (amt) gene promoter activity. Isoforms of pin1

XX and amt gene promoters are useful in manipulating expression of genes,

XX particularly in transformed plant cells. The gene promoters are useful in

XX constructing gene expression vectors and in Controlled Environmental

XX Agriculture for heterologous protein production. The vectors are useful

XX in facilitating the expression and/or secretion of heterologous proteins

XX in cell culture or by crop cultivation. The new gene promoter isoforms

XX provide high level, stable and controllable expression that is

XX temporally, environmentally, or developmentally regulatable. This

XX sequence represents a potato pin1 gene promoter isoform

XX SQ Sequence 1546 BP; 501 A; 270 C; 284 G; 490 T; 0 U; 1 Other;

Query Match 86.2%; Score 1375.2; DB 6; Length 1546;

Best Local Similarity 94.8%; Pred. No. 7.6e-293;

Matches 1469; Conservative 0; Mismatches 74; Indels 9; Gaps 4;

QY 49 ATCTTTGTTTGAATAAATTTGAAAGAAAGCTAGGACCATGACCTTGGGTGCAACAAT 108

DB 1 ATCTTTGTTTGAATAAATTTGAAAGAAAGCTAGGACCATGACCTTGGGTGCAACAAT 60

QY 109 ATGTTGTCCTCAATGTTGTTACAGGATTTGTTACATCTCCGGGTACTTTAAGTTGAC 168

DB 61 ATGTTGTCCTCAATGTTGTTACAGGATTTGTTACATCTCCGGGTACTTTAAGTTGAC 120

QY 169 CAGGGCATTCACCATTTATATTGCGTGCATTAATTTGTTGGCATTTCCCTCCACTTG 228

DB 121 TAGGACATTCACCATTTATATTGCGTGCATTAATTTGTTGGCATTTCCCTCCACTTG 180

QY 229 GATTTAGTCGGGGGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGCCCCAGA 288

DB 181 GATTTAGTCGGGGGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGCCCCAGA 240

DB 361 CATCGAAGTTACATCAGTACGACCCCATATACGTGCCATCGTAGTCCCTTAGCGCAT 420

QY 469 CAATGACCCACATTTGGCCCGGATCGAAACGTCGG-CACCCCGCTTTCGGGTTCGATGCGG 527

DB 421 CAATGACCCACGTTTGGCTCGATCGAGACGTCGGCCACCGCTATCGGGTTCGATGCTG 480

QY 528 CCCAAACGATGTATCGACAGTTGTTGCGTACTCGATAGTGGCAGCATAAAGTGAATCA 587

DB 481 CCCAGACGCTGATGGAAGTGTGTCGATGCTCGATAGTGGCAGCATAAAGTGAATCA 540

QY 588 CAAAAGCAAGAGGAGGAGAAACAAAAGAAAGATCTCAAGTAGCCCATGTTTGTGAAATTT 647

DB 541 CAAAAGCAAGAGGAGGAGAAACAAAAGAAAGATCTCAAGTAGCCCATGTTTGTGAAATTT 600

QY 648 ATATGTGACAAATTTATTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCACTA 707

DB 601 ATATGTGACAAATTTATTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCACTA 660

QY 708 CGGATATTAAATCGTATTATATAGCAATATATATCTTGGTAAATTTATATAAGCAATATAT 767

DB 661 TGGATATTAAATCGTATTATATAGCAATATATATCTTGGTAAATTTATATAAGCAATATAT 720

QY 768 TACAATATGATTTGGTAAACGTTGAGGTGGAAATCTATAAGAGCCGCTTAATAATTA 827

DB 721 TACAATATGATTTGGTAAACGTTGAGGTGGCAAAATGTATAAGAGCCGCTTAATAATTA 780

QY 828 TTATTTATGATTAATAGCTATAGTACAGTAACTTTATTTGGTAAATTTATATAAGCAATATAT 887

DB 781 TTATTTATGATTAATAGCTATAGTACAGTAACTTTATTTGGTAAATTTATATAAGCAATATAT 840

QY 888 ATAAACTCTGTAACGTCGACCGAAATTTTCTTAAACCTAAATATTTAAAGCAGACTATTTT 947

DB 841 ATAAACTCTGTAACGTCGACCGAACTTTTCTTAAACCTAAATATTTAAAGCAGACTATTTT 900

QY 948 CAGATTTTTCGTGGCCAAAGTTTCTTGCATCTACTATCTAGCCCATTTTACTTTATCTG 1007

DB 901 AATATTTTTCGTGGCCAAAGTTTCTTGCATCTACTATCTAGCCCATTTTACTTTATCTG 960

QY 1008 TTCTAGCTCTTAGGTACAGCTTTGAACATATAAAATTCATAAAATTTGAAAGTAAATAAT 1067

DB 961 TTCTAGCTCTTAGGTACAGCTTTGAACATATAAAATTCATAAAATTTGAAAGTAAATAAT 1020

QY 1068 AGTTTTTTTTTTCATATTAATCTCGTAGGATCAATTTGTTAGATCAATCTGAATAATACAA 1127

DB 1021 AG-----TTTTTTTTTTCATATTAATCTCGTAGGATCAATTTGTTAGATCAATCTGAATAATACAA 1077

QY 1128 ACCATTCTGATTTTAAATCACAACCATCTCGCAAGGGGAAGTCTAT---GTGATCCGT 1184

DB 1078 ATCATCTGATTTTAAATTCATTAATCTCGATGATGGGAACGCTATGTTGGTATCGT 1137

QY 1185 GACAAGTGGTTGATTTATTTCTTAGTCTTAGATTGGATGCAAACTTTTAGTGCAAAATATCT 1244

DB 1138 GACAAGTGGTTGATTTATTTCTAAGTCTGGATTGGAGTCACAACTTTTAGTGCAAAATATCT 1197

QY 1245 ATTAAGAGAACCCCTATTGATGCARATATCTATTAAGAACCCCTATTTCATGCTTTAT 1304

DB 1198 ATTAAGAGAACCCCTATTGATGCARATATCTATTAAGAACCCCTATTTCATGCTTTAT 1255

QY 1305 TATTTTTCGATCGGAGCATGGATATTTTACTTAATTAATAAATTTGAAAGCAATTTGAT 1364

DB 1256 TATTTTTCGATCGGAGCATGGATATTTTACTTAATTAATAAATTTGAAAGCAATTTGAT 1315

QY 1365 CGACAGTCAATCAAGCTTATCGTCGATCCACATTAATAAATTAAGTATGCTGCTTTT 1424

DB 1316 CGACAGTCAATCAAGCTTATCGTCGATCCACATTAATAAATTAAGTATGCTGCTTTT 1375

QY 1425 AGAAGAACCAAGTGGATCATGTATATTTTAGTATTAATAATCTCTTATATAATCTATAT 1484

DB 1376 AGAAGAACCAAGTGGATCATGTATATTTTAGTATTAATAATCTCTTATATAATCTATAT 1435

QY 1485 ATACCTCTTAAACTAAATGCTATCAACAAATATAAACTTAGATTTCTTTAAAGAA 1544

Db 1436 ATACCTCTAAACTAAATGCACTCTAACACACAAATATAAATAGATCTTTTAAAGAA 1495
 Qy 1545 TTGCAGAAATTAATGGAGGCAATTAAGTCTATGTTGAAGTTGGTTGCTTTC 1595
 Db 1496 TTGCAGAAATTAATGGAGGCAATTAAGTCTATGTTGAAGTTGGTTGCTTTC 1546

RESULT 4
 AAV52754/c
 ID AAV52754 standard; DNA; 3033 BP.
 XX AC
 XX AAV52754;
 XX
 XX 02-NOV-1998 (first entry)
 XX
 XX Nicotiana tabacum osmotin gene with promoter.
 XX
 XX Nicotiana tabacum; tobacco plant; osmotin gene; promoter; inhibition;
 KW fungal pathogen; insect pathogen; nematode pathogen; viral pathogen; ds.
 XX
 XX Nicotiana tabacum.
 XX
 XX Key Location/Qualifiers
 FH 2034..2774
 FT /*tag= a
 FT /product= "osmotin"
 FT /transl_except= (pos:2574..2576,aa:Arg)
 XX
 XX US5801028-A.
 XX
 XX 01-SEP-1998.
 XX
 XX 07-JUN-1995; 95US-00482037.
 XX
 XX 20-MAY-1993; 93US-00065147.
 PR 12-JAN-1994; 94US-00180428.
 XX
 XX (PURD) PURDUE RES FOUND.
 XX
 XX Hasegawa PM, Bressan R;
 PI
 XX
 XX WTI; 1998-494773/42.
 DR P-PSDE; AAW69751.
 XX
 XX Inhibition of pathogens in plants by recombinant expression of pathogen
 PT inhibiting proteins - uses nucleic acid constructs containing the
 PT pathogen inhibiting proteins under control of osmotin promoter, which is
 PT inducible by specific signals.
 XX
 XX Claim 1; Col 29-34; 26pp; English.
 PS
 XX A method has been developed of inhibiting a pathogen in a plant. The
 CC method comprises: (a) providing or constructing a vector comprising an
 CC osmotin promoter and foreign DNA sequence encoding a pathogen-inhibiting
 CC protein, where the promoter is operably linked to the foreign DNA
 CC sequence and includes: (i) nucleotide sequence 5' of the osmotin coding
 CC sequence extending to position -248 bases from the start of the osmotin
 CC protein coding sequence, the coding sequence defined as starting at bp
 CC 2034 of the 3033 bp osmotin sequence (present sequence), (ii) a
 CC nucleotide sequence which hybridises to (i) and promotes expression of an
 CC operably linked coding sequence under conditions of desiccation; and (b)
 CC introducing the vector into the plant to create a transformed plant,
 CC where expression of the pathogen-inhibiting protein in the transformed
 CC plant is regulated by the osmotin promoter. The method is useful for the
 CC production of recombinant plants having genes under control of an osmotin
 CC promoter, especially of pathogen inhibiting proteins. Osmotins are
 CC cationic plant proteins, similar to tobacco PR-5-type proteins. The
 CC osmotin genes are under control of hormonal or environmental signals,
 CC including abscisic acid, ethylene, tobacco mosaic virus infection,
 CC salinity, desiccation and wounding. The present sequence represents the
 CC Nicotiana tabacum osmotin gene with promoter
 XX
 XX Sequence 3033 BP; 973 A; 505 C; 547 G; 1008 T; 0 U; 0 Other;

Query Match 30.0%; Score 479.2; DB 2; Length 3033;
 Best Local Similarity 76.9%; Pred. No. 1.4e-95;
 Matches 678; Conservative 0; Mismatches 163; Indels 41; Gaps 6;

Qy 46 GGTATCTTTGTTTGAAGAAATTTGAAAGAGCTAGGACCAATGAGCTTGGGTGCAAC 105
 Db 2622 GGCATCTTTGTTTGAAGAAATTTGAGAAATATGTAGGACCAAGGTCTCTGTGTGCAAC 2563
 Qy 106 AATATTGTTGCTCTCAAAATGTGTACAAAGGATCTTACATCTCTCCGGGTACTTTAAAGTT 165
 Db 2562 AATATTGTTGCTCTCGAATGTAGTACAAAGGTTATATACATCTCTCCGGGAACCTTAAGTT 2503
 Qy 166 GACCAGGGCAATTCACATTTATTTTGGCGTCAATGAATGTGTGGCAATTCCTCCAC 225
 Db 2502 CGCGGGGACATTCGCGCTTTATATTAGCGTACATGAATGTGATGTCATTCCTCCAC 2443
 Qy 226 TTGGATTAGTGGCGGAAAGTCATCGGTATATTAATCCATCACTAAAGAAATGTCCC 285
 Db 2442 TAGGGTTAGTGGCGGAAAGTCATCGGAATGTTGAATCCATCACTAAAGAAATGTCCC 2383
 Qy 286 AGAAATCTAAGTTGTTGAATCTGGTCCAAAGGGCTACTCGGCTAGGTTGTTGGTGTTCG 345
 Db 2382 AGAAATCTAAGTTGTTGAATCTGGTCCAAAGGGCTACTCGGCTAGGTTGTTGGTGTTCG 2323
 Qy 346 CCCACCGGTGCACTGCGAGGACACCAACATCACTGACAGTCAATGACGACCTCTACAG 405
 Db 2322 CCCACCGGTGCACTGCTAGGACTCCACCACTGACCGGTTGGCACGCTACCCCTACCAG 2263
 Qy 406 CACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCGCATCTAGTGCCTTAGCGG 465
 Db 2262 CAGCATTTGAAGTTACAATTAGTACGCGCCCATACACGTGCCATTTTAGTACCTCGTGGG 2203
 Qy 466 CATCAATGACCCACATTTTGGCGCCGATCGAAACGTCGG-CHACCGCTTTTGGGGTGGATG 524
 Db 2202 CATTGATCACCACAGTTTGGCGCTCGATCGAGACGCGCCGCTATGGTGTGTCGAG 2143
 Qy 525 CGGCCCAACAGTGTATGACAGTTGTTGGTGTGCTGACCTGACGTAGTGCAGCATAGTGAAG 584
 Db 2142 CGGCCCAACAGTGTATGACAGTTGTTGGTGTGCTGACCTGACGTAGTGCAGCATAGTGAAG 2083
 Qy 585 TCACAAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCAATGTTGTGTGAAA 644
 Db 2082 TCACCAAGGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTTGCCCATGTTGTGTGGACA 2023
 Qy 645 TTTATATGTGGACAATTTATTTTGGTACT-----TTATATATAGG 685
 Db 2022 TTTTATTAACAAGTTGGGTTGTTGGATATAGTGACAAATTTGTTAGTGGTTTATATAGG 1963
 Qy 686 GATATGGCGGCTTTTGGCACTACGGATATTAATCGTATTATATAGCAATATCATCTTTG 745
 Db 1962 GGAATGGCGGCTTTTGGTACTATGATATTAATC-----ATAAATATTTTAAATTTG 1908
 Qy 746 ACTAATTTAAACGAAATATATTAATATGATTTTGGTAAACGTTGAGGTGG-AAAAATG 804
 Db 1907 ACTA---ATAAACGGATATATCTCAAGGATGCTTTGGCAAGATGAGGCGCGCTTAAA 1851
 Qy 805 TATAAGACCGCTTAATAATTAATTTATTTATGAATATAGCTATAGTTACAAAGTTAACT 864
 Db 1850 CATAGAGCGGCTTAATAATTTATTTATTTATGATATAG-----AAGTCAAT 1803
 Qy 865 TTATTGTTGATTAATTTGACATATAAATCTCTGTAACGTGAC 906
 Db 1802 TTATTGTTGATTAACGCTGACCTATAAATCTCTGTAACGTGAC 1761

RESULT 5
 AAX16340/c
 ID AAX16340 standard; DNA; 3033 BP.
 XX AC
 XX AAX16340;
 XX
 XX 26-APR-1999 (first entry)

XX DE Tobacco osmotin gene and non-transcribed 5' flanking sequence.
 XX KW Nicotiana tabacum; tobacco; osmotin; promoter; ds.
 XX OS Nicotiana tabacum.
 XX FH Key Location/Qualifiers
 XX CDS 2034..2774
 XX FT /*tag= a
 XX FT /trans_except= (pos:2574..2576,aa:Arg)
 XX PN US5874626-A.
 XX XX 23-FEB-1999.
 XX PF 12-JAN-1994; 94US-00180428.
 XX PR 20-MAY-1993; 93US-00065147.
 XX XX (PURD) PURDUE RES FOUND.
 XX PA Hasegawa PM, Bressan R;
 XX PI WPI; 1999-180080/15.
 XX DR P-PSDB; AAW94510.
 XX XX Tobacco osmotin gene promoter - and recombinant construct comprising
 XX PT foreign gene under its control.
 XX PS Claim 1; Fig 9A; 26pp; English.
 XX CC The present sequence represents the DNA sequence comprising the Nicotiana
 CC tabacum (tobacco) osmotin gene and non-transcribed 5' flanking (promoter)
 CC sequence. The present invention specifically claims a DNA fragment
 CC comprising the osmotin gene promoter sequence with no more than 100 bp of
 CC the coding sequence. Also described are methods which are useful in
 CC processes for achieving expression of a coding sequence from a foreign
 CC gene in a host cell
 XX SQ Sequence 3033 BP; 973 A; 505 C; 547 G; 1008 T; 0 U; 0 Other;
 Query Match 30.0%; Score 479.2; DB 2; Length 3033;
 Best Local Similarity 76.9%; Pred. No. 1.4e-95;
 Matches 678; Conservative 0; Mismatches 163; Indels 41; Gaps 6;
 QY 46 GGTATCTTTTGGAAAAATTCGAAAGACGATAGACACATGACCTTGGTGCAC 105
 DB 2622 GGCATCTTTTGGAAAAATTTTGGAAAAATTTAGGACCAAGGTCTTGTGTGCAAC 2563
 QY 106 AATATTGTTCTCCAAATGCGTACAGGATTTTACATCTCCGGGTACTTTAAGTT 165
 DB 2562 AATATTGTTCTCCGAATGATACAGGTTTATACATCTCCGGGAACCTTAAGTT 2503
 QY 166 GACACGGCATTCACATTTATTTTCCGCGTGAATTTGTTGGCAATTTCCCTCCAC 225
 DB 2502 CGCGGGGACATTCGCGCTTTATATTAGCCGTACAATGAATTTGCATGGCATTTCCCTCCAC 2443
 QY 226 TTGGATTAGTCGGGGGAAAGTTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCC 285
 DB 2442 TAGGTTAGTCGGGGGAAAGTTCATCGGATTTGATTCATCACTAAAGAAATGTCCC 2383
 QY 286 AGAAATCTAAAGTTTGTGAATCTGCAAGCGTACTCGGCTAGGTTGTTGGTTTGC 345
 DB 2382 AGAAATCTAAACACATCAATTTGTTCCAAAGCGTATTTCAGCAAGGTGTTTGGTTTAC 2323
 QY 346 CCCACCGGTGCACTGACGACACACCAATCACCAGTCATGACGACCTCTACACAG 405
 DB 2322 CCCACCGGTGCACTGATGAGACTTCCACACAGTCACCGGTTTGGACAGTACCCCTACACAG 2263
 QY 406 CACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATCGTACGTCCTAGGCG 465
 DB 2262 CAGCATTTGAAGTTACAATTTAGTACGCGCCCATACACAGTGCATTTTAGTACCTCGTGGCG 2203

QY 466 CATCAATGACCCACATTTGGCCCCGATCGAAACGTGG-CACCGGCTTTTCGGGGTGGATG 524
 DB 2202 CATTGATCACCCAAAGTTTGGCTCGATCGAGAGCGCCGCCACCGCTTATGGGTGTCGACG 2143
 QY 525 CCGCCCAACGATGATGAGACAGTTTGGTACCTCGATAGTGGCAGCATAGTGAAG 584
 DB 2142 CCGCCCAACGATGATGAGACAGTTTGGTACCTCGATAGTGGCAGCATAGTGAAG 2083
 QY 585 TCACAAAAGCAAGAGGAGGAGAAACAAAGAAAGATCTCAAGTAGGCCCATGTTTGTGAAA 644
 DB 2082 TCACCAAGGCAAGGAGGAGGAGAAACAAAGAAAGATCTCAAGTTGCCCATGTTGTTGACA 2023
 QY 645 TTTATATGTGGACAAATTTTGTGGTACT-----TTATATATAGG 685
 DB 2022 TTTTATTAACAAGTTGGGTTTGGATATAGTACAAATTTGTAGTGGTTTATATAGG 1963
 QY 686 GATATGGCGGCTTTTGGCACTACGATATTAATCGTATTATATAGCAATATCATACTTTG 745
 DB 1962 GGAATGGCGGCTTTTGGCACTACGATATTAATCGTATTATATAGCAATATCATACTTTG 1908
 QY 746 ACTAATTATAAACGAAATATATATACAAATATGATTTGGTAAACGTTGAGTGG-AAAAATG 804
 DB 1907 ACTA---ATRAACGGATATATCTCAAGGATGCTTTGGCAAGATGGAGGCGGCGCTTAAA 1851
 QY 805 TATAAGGCGGCTTAATAATTAATTTATTTATGAATATAGCTATAGTTACAAGTTAACT 864
 DB 1850 CATAGAGCGGCTTAATAATTAATTTATTTATGAATATAG-----AAGTCAAT 1803
 QY 865 TTATTGGTGATAACTTTTGACATATAAACTCTGTACGTGAC 906
 DB 1802 TTATTGGTAAATACGCTGACCTATAATCTCTGTACGTGAC 1761
 RESULT 6
 AAQ15269/c
 ID AAQ15269 standard; cDNA; 883 BP.
 XX AC AAQ15269;
 XX DT 25-MAR-2003 (revised)
 DT 16-MAR-1992 (first entry)
 XX DE Osmotin-like antifungal protein.
 XX KW tobacco; osmotic tolerance; ss.
 XX OS Nicotiana tabacum.
 XX FH Key Location/Qualifiers
 XX CDS 17..757
 XX FT /*tag= a
 XX FT /note= "osmotin-like"
 XX PN EP460753-A.
 XX XX 11-DEC-1991.
 XX PF 31-MAY-1991; 91EP-00201344.
 XX PR 07-JUN-1990; 90NL-00001293.
 XX PA (MOGE-) MOGEN INT NV.
 XX PI Woloshuk CP, Melchers LS, Cornelisse BJ, Meulenhoff BJ;
 PI Selabuurla MB, Vandenberg PJ;
 XX DR WPI; 1991-363235/50.
 XX DR P-PSDB; AAR15660.
 XX PT New antipathogenic proteins obtd. from plants - obtd. by inducing
 XX resistance in plant to pathogen and pregn. of extract from plant.

PS Claim 18; Page 17; 25pp; English.

XX The full-length cDNA clone encoding antifungal protein AP20 was obtained
 CC from a lambda ZAP cDNA library prepared from tobacco mosaic virus-
 CC infected Samsum NH tobacco leaves. The library was screened with a probe
 CC for sequences homologous to the NP24 gene of tomato. One positive clone
 CC was found to contain the complete coding sequence for osmotin except for
 CC the A-T dinucleotide of the translation initiation codon. With the use of
 CC PCR, a BamHI site and an A-T dinucleotide was introduced in front of the
 CC osmotin cDNA; behind the gene a BamHI site was introduced. See also
 CC AAQ15270. (Updated on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 883 BP; 220 A; 198 C; 205 G; 260 T; 0 U; 0 Other;

Query Match 27.0%; Score 430.2; DB 2; Length 883;
 Best Local Similarity 84.1%; Pred. No. 6.4e-85;
 Matches 497; Conservative 0; Mismatches 93; Indels 1; Gaps 1;

Qy 46 GGTATCTTTGTTTCAAAAAATTGAAAAGACGTAGGACACATGGACCTTGGGTGCAAC 105
 Db 605 GGCACTTTGTTTGAATAATTTTGAHAATAATGTAGGACCAACAGGTCTTGTGTGCAAC 546

Qy 106 AATATTGTTGTCCTCCAAATGTGTCACAAAGATTGTTACATCTCCGGGTACTTTAAAGTT 165
 Db 545 AATATTGTTGTCCTCCGAATGTAGTACAAGGGTTATTACATCTCCGGGAACCCCTAAGTT 486

Qy 166 GACCAGGGCATTCACCATTTATATTTCGCCGTGCATTGNAATGTTGTGGCATTTCCCTCCAC 225
 Db 485 CGCGGGGACATTCGCGGTTTATATTAGCCGTACAAATGAATTGCATGGCAATTTCCCTCCAC 426

Qy 226 TTGATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCCATCAACTAAAGAAATGTCCC 285
 Db 425 TAGGTTAGTCGGGGCGAAAGTCATCGGAATGTTGAATCCATCAACTAAAGAAATGTCCC 366

Qy 286 AGAAATCTAAGTTGTTGAACCTGCTCCAAAGCGCTACTCGGCTAGGGTGTTTGGTGGTTTC 345
 Db 365 AGAAATCTAAACCACTGAATTTGGTCCAAAGCGTATTACGCCAAGGTGTTTGGTGGTTTAC 306

Qy 346 CCCACCCGGTGCACTGCAGGACACACCACCAATCACCAGTCATGCACGAACCTCTACCAG 405
 Db 305 CCCACCCGGTGCACTGTAGGACTCCACCAAGTCACCGTTTGGCAGCTACCCCTACCAG 246

Qy 406 CACCATCGAAGTTACATCCAGTAGAGACCCCATATACCTGCCCATCGTAGTGCCCTTAGGCG 465
 Db 245 CAGCATTTCAAGTTACAATTAGTAGGGCCCCCATACACGTGCCAATTTTAGTACCTCGTGGCG 186

Qy 466 CATCAATGACCCACATTTGGCCCCCGATCGCAACGTCGG-CACCCGCTTTTCGGGGTCGATG 524
 Db 185 CATTGATCACCCAAGTTTGGGCTCGATCGAGACGCCGCCACCGCCTATGGGTGTGACG 126

Qy 525 CCGCCCCAAACGATGTATGCACAGTTGTTGCGTACCTCGATAGTGCGCAGCATAAAGTGAAG 584
 Db 125 CCGCCCCAAACGGTGTAGCGACAGTTGTTTGGACCTCGATAGTGGCAGCATAAAGTATAAG 66

Qy 585 TCACAAAAGCAAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCAATGT 635
 Db 65 TCACAAAGGCAAGGAGGAGAAACAAAGAGATCTCAAGTTGCCCAATGT 15

RESULT 7
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 ID AAQ15270 standard; DNA; 884 BP.
 XX
 AC AAQ15270;
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 16-MAR-1992 (first entry)
 XX
 XX
 DE Encodes C-terminally truncated osmotin-like antifungal protein.
 XX tobacco; osmotic tolerance; AP20; ss.
 XX Nicotiana tabacum.
 OS

RESULT, T 7

AAQ15270/c	
ID	AAQ15270 standard; DNA; 884 BP.
XX	
XX	
AC	AAQ15270;
XX	
XX	
DT	25-MAR-2003 (revised)
DT	16-MAR-1992 (first entry)
XX	
XX	
DE	Encodes C-terminally truncated osmotin-like antifungal protein.
XX	
XX	
KW	tobacco; osmotic tolerance; AP20; ss.
XX	
OS	Nicotiana tabacum.

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<p>Query Match 12.4%; Score 197.8; DB 3; Length 906; Best Local Similarity 61.6%; Pred. No. 9e-34; Matches 375; Conservative 0; Mismatches 217; Indels 17; Gaps 3;</p>					
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DB	619	GGCATCTCTGCTTAAAGAAATCTTGAGTAGTCAGTATCGTACATGATCCCTGACCGGTGC 560			
QY	100	TGCAACAATATTGTTGCTCCTCCAAATGTTGTAAGAGATTGTTACATCTCCGGGTACTT 159			
DB	559	TACAACAGTATTGTTGCTGCTGTAATACAGTACACGGGTTGTTGCATCCACCTGGGCTC 500			
QY	160	TAAGTTGACAGGGCATTACCATTTATTTGCGGTGCAATGTAATGTTGGCAATTC 219			
DB	499	TCAACAGCTTTGGACATTTGTCGTTTATGTCGCGGTACATAGTATCCGATGGCAGTTC- 441			
QY	220	CTCCACTTGGATTAGTCGGGGCGAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAA 279			
DB	440	-----GAACTAGTTGGGCTAAATCCATAGTATGTTAAATCCATCCACAGTGAGA 389			
QY	280	TGTCCCGAAATCTAAGTTGTTGAACTGGTCCAGGGCTACTCGGTAGGGTGTGGTG 339			
DB	388	TATCGTAAAGTCTAAGTTGTTGAAATTTGTTTCAAGGCTACTCAGCCACGTTGTTGGTG 329			
QY	340	GTTTGGCCCGCCCGTGCACCTGGAGGACACACCAATCACCAGTCATCGACGACCTC 399			
DB	328	GGTGTCCCGCCAGTACATTTGGAGTCCACACTGTCAGTCACAGTTTGGCATTCGGCCAC 289			
QY	400	TACCAGCACCATCGAAGTTATCCAGTACGACCCCATATACCTGCCATCGTAGTCCCC 459			
DB	268	GACCTGAGGAGTCAAAGTTTCAATTTGGTCTCTACCCCAATCCCGTGCATTTTAGTCCCG 209			
QY	460	TAGGGGATCAATGACCCCATTTGGCCCGCATGGAACGTCGCGCACCGCTTTCGGGT 519			
DB	208	CCGGACATCTAGCCTCCATGATTGGCCAGCATCTAGAGTCGG--CCACCTCCAGGGCT 151			
QY	520	CGATSCCGCCCAACGATGATGGACAGTTGTTGGCTACCTCGATAGTGGCAGCATAAGT 579			

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Db 150 TGGCGCACCCACACAGGTTGAACATACATGTTTGGATTTCGAATTCGAGCGGTGTTGC 91
QY 580 GAAGTCAAAAGCAAGAGGGAGAAACAAAAGAGATCTCAAGTAGCCCATGTTTGT 639
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QY 640 TGAATTTA 648
Db 30 TTAGTTCTA 22

RESULT 11
AAC47227/c
ID AAC47227 standard; DNA; 902 BP.
XX
AC AAC47227;
XX
DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 53029.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
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PR	28-OCT-1999;	99US-0161922P.	Db			
PR	28-OCT-1999;	99US-0161933P.				
PR	29-OCT-1999;	99US-0162142P.				

Query Match 12.3%; Score 196.2; DB 3; Length 902;
 Best Local Similarity 61.4; Pred. No. 2e-33;
 Matches 374; Conservative 0; Mismatches 218; Indels 17; Gaps 3;

RESULT 12
 ABZ14313/c
 ID ABZ14313 standard; DNA; 735 BP.
 XX
 AC ABZ14313;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2118.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 FN WO200216655-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001WO-US026685.
 XX
 PR 24-AUG-2000; 2000US-0227866P.
 PR 26-JAN-2001; 2001US-0284647P.
 PR 22-JUN-2001; 2001US-0300111P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PI Harper JF, Krebs J, Wang X, Zhu T;

Db 355 TATCGTAGAAGTCTAAGTTGTTGAATTGTTTCAAAGCGTACTCAGCCAAAGTGTGTTGGTG 296
 Qy 340 GTTTCGCCCCACCGGTGCACGTGACGAGGACACCAACACATCAGCAGTTCATGCAAGAACCTC 399
 Db 295 GCTGTCCCGCAGCGAGTACATTTGGAGTCCACCACTGCAGTACCAAGTTGGCATCGGCCAC 236
 Qy 400 TACCAGCACCATCGAAGTTACATCCAGTACGACGCCCATATACCTTGCCATCGTAGTGCCCC 459
 Db 235 GACCTGAGGAGTCAAAGTTCAATTTGGTCTTACCCCAATCCGTCATTTAGTGCCCG 176
 Qy 460 TAGCGGATCATGACCCACATTTGGCCCGATCGAAACGTGCGCACCCCGCTTTCGGGGT 519
 Db 175 CCGGACATCTAGGCTCCATGTTGGCCAGCATCTAGACGTCGG--CCACCTCCAGGGCT 118
 Qy 520 CGATCGCGCCCAACGATGTATGACAGTGTGTCGCTACCTCGATAGTGGCAGCATAGT 579
 Db 117 TCGCGACGCCACAGGTGTAACATGATGTTTGGATTTGATGTTGGCGTGTTC 58
 Qy 580 GAAAGTCAAAAAGCAAGGAGGAGAAACAAAGAGAGATCTCAAG 625
 Db 57 GGTGGAGATGACAAAAGTCCGGAATATCAAAAGTAGAGACCAAG 12

RESULT 14

ADA68525/c
 ID ADA68525 standard; DNA; 735 BP.

XX AC ADA68525;

XX AC 20-NOV-2003 (first entry)

XX DE Arabidopsis thaliana gene, SEQ ID 566.

XX KW Plant; bacterial infection; fungal infection; viral infection; ds.

XX OS Arabidopsis thaliana.

XX PN WO2003000898-A1.

XX PD 03-JAN-2003.

XX PF 22-JUN-2001; 2001WO-IB001105.

XX PR 22-JUN-2001; 2001WO-IB001105.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.

XX PT Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.

XX PS Claim 6; SEQ ID NO 566; 899pp; English.

XX CC The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.

XX SQ Sequence 735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;

XX Query Match 12.3%; Score 195.6; DB 7; Length 735;

Best Local Similarity 62.3%; Pred. No. 2.6e-33;
 Matches 365; Conservative 0; Mismatches 204; Indels 17; Gaps 3;

Qy 46 GGTATCTTTGTTGAAAAAATGGAAAAAGAGTGGAGACCATG-----GACCTTGGG 99
 Db 586 GGCATCTCTGCTTAAAGAAATCTTGAGTACTCAGTACTGCTACATGATCCCTGACCGTTTCG 527
 Qy 100 TCGAACAAATTTGTTGCTCCTCAATGTTGTTACAGAGTTGTTACATCCTCGGGTACTT 159
 Db 526 TACAACAGTATTGGTTCGTTCTGTAATACAGTACACGGGTTGTTGCATCCCTCGGGGTC 467
 Qy 160 TAAAGTTGACCCAGGCAATTCACCAATTTATATTGTCGCTGCAATTTGAATTTGTGGCAATTC 219
 Db 466 TCACACAGTTGGACATTTGTCGTTTATGTTCTCGGTACATAGTATCGATGGCAGTTC- 408
 Qy 220 CTCCTACTTGGATTTAGTTCGGGGGAAAGTCACTCGGTATATTAATCCATCAACAAAGAA 279
 Db 407 -----GAAGTAGTTGGGCTAAACTCCATAGGTATGTTAAATCCATCGCAAGTGAGA 356
 Qy 280 TGTCCCGAGAAATCTAAAGTTGTTGAACCTGCTCCAGGGGTACTCGGCTAGGTTGTTGGTG 339
 Db 355 TATCGTAGAGTCTAAGTTGTTGATTTGTTTCAAGGTACTCAGCCAAACGTTTGGTG 296
 Qy 340 GTTTCGCCCCACCGGTGCACGTGACGAGCACCAACCAATCAACAGTATGACCAAGCTC 399
 Db 295 GCTGTCCCGCAGCCAGTACATTTGGAGTCCACCACTGCAGTACCAAGTTGGCATCGGCCAC 236
 Qy 400 TACCAGCACCATCGAAGTTACATCCAGTACGACGCCCATATACCTGCGCATCGTAGTGCCCC 459
 Db 235 GACCTGAGGAGTCAAAGTTTCAATTTGGTCTTACCCCAATCCGTCATTTAGTGCCCG 176
 Qy 460 TAGCGCATCAATGACCCACACATTTGGCCCGCATCGAAACGTGCGCACCCCGCTTTCGGGGT 519
 Db 175 CCGGACATCTAGCCTCCATGATTTGGCCAGCATCTAGACGTCGG--CCACCTCCAGGGCT 118
 Qy 520 CGATCGCGCCCAACGATGTATGACAGTGTGTTGCGTACCTCGATAGTGGCAGCATAGT 579
 Db 117 TCGCGACGCCCACACCGGTGTAACATGATGTTTGGATTTGCAATTTGCGAATTTGCGGGCTGTTGC 58
 Qy 580 GAAAGTCAAAAAGCAAGGAGGAGAAACAAAGAGAGATCTCAAG 625
 Db 57 GGTGGAGATGACAAAAGTCCGGAATATCAAAAGTAGAGACCAAG 12

RESULT 15

ABN98566/c
 ID ABN98566 standard; DNA; 950 BP.

XX AC ABN98566;

XX DT 01-AUG-2002 (first entry)

XX DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 334.

XX KW Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
 KW disease; crop; thale cress; tolerance factor; insect; pathogen;
 KW nutrition; ds.

XX OS Arabidopsis thaliana.

XX PN US2002023281-A1.

XX PD 21-FEB-2002.

XX PF 26-JAN-2001; 2001US-00770445.

XX PR 27-JAN-2000; 2000US-0178472P.

XX PA (GORL/) GORLACH J.

XX PA (ANY/) AN Y.

XX PA (HAMI/) HAMILTON C M.

XX PA (PRIC/) PRICE J L.

XX PA (RAIN/) RAINES T M.

PA (YUYV//) YU Y.
PA (NAME//) RAMEAKA J G.
PA (PAGE//) PAGE A.
PA (MATH//) MATHW A V.
PA (LEDF//) LEDFORD B L.
PA (WOES//) WOESSNER J P.
PA (HAAS//) HAAS W D.
PA (GARC//) GARCIA C A.
PA (KRIC//) KRICKER M.
PA (SLAT//) SLATER T.
PA (DAVI//) DAVIS K R.
PA (ALLE//) ALLEN K.
PA (HOFF//) HOFFMAN N.
PA (HURB//) HURBAN P.
XX
PI Grolach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX
DR WPI; 2002-403163/43.
XX
XX New Arabidopsis thaliana nucleic acid for identifying homologous genes,
PT producing compositions that modulate the expression or function of its
PT encoded protein, and mapping functional regions of protein.
XX
PS Claim 1; SEQ ID NO 334; 49pp + Sequence Listing; English.
XX
XX The invention relates to an Arabidopsis thaliana nucleic acid (I)
CC comprising a sequence capable of hybridising under stringent conditions
CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
CC given in the specification or its fragment. A polypeptide (II) encoded by
CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
CC useful for screening a candidate agent for its biological effect. (I) is
CC useful in identifying homologous or related genes, in producing
CC compositions that modulate the expression or function of its encoded
CC protein, mapping functional regions of the protein and in studying
CC associated physiological pathways. (I) is also useful for the genetic
CC manipulation of cells, particularly plant cells. (I) is also useful in
CC screening assays of various plant strains to determine the strains that
CC are best capable of withstanding a particular disease or environmental
CC stress. (II) and (III) are useful for screening of biologically active
CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
CC pathways. The screened agents are useful in improved methods of treating
CC crops to prevent or treat disease. (II) are also useful in screening
CC programs to identify agents that mimic or enhance the action of tolerance
CC factors. Such agents are useful in improved methods of treating crops to
CC enhance their tolerance to environmental stress. (I) is also useful for
CC enhancing or inhibiting production of a biosynthetic product in a plant.
CC (III) is useful for identifying other mediators that may induce
CC expression of proteins of interest, for establishing the extent to which
CC any specific insect and/or pathogen is responsible for damage to a
CC particular plant, for identifying other mediators that enhance or induce
CC tolerance to environmental stress, for identifying factors involved in
CC biosynthetic pathways of nutritional, commercial, or medicinal value and
CC for identifying productions of nutritional, commercial or medicinal
CC value. (IV) is useful in the study of genetic function and regulation,
CC for alteration of the cellular metabolism and for screening compounds
CC that may affect the biological function of the gene or gene products.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docID=999909770445
XX
SQ Sequence 950 BP; 261 A; 225 C; 213 G; 251 T; 0 U; 0 Other;
Query Match 12.3%; Score 195.6; DB 6; Length 950;
Best Local Similarity 62.3%; Pred. No. 2.8e-33;
Matches 365; Conservative 0; Mismatches 204; Indels 17; Gaps 3;
XX
QY 46 GGATCTCTTTGTTGAAAGAAATGGAAAGAACCTAGGACCAATG-----GACCTTGGG 99
DB 594 GGCATCTCTGCTTAAAGAAATCTTGAGTACTGCTAGTATCGTATCATGATCCCTGACCGTTCG 535

QY 100 TGCACAAATATTGTTGTCCTCCAAATGTTGGTCAAGAGATTGTTACATCTCCGGGTACTT 159
DB 534 TACACAGATTATTGGTTTCGTCTGAAATACAGTACACGGGTTGTTGCATCCACCTCGGGCTC 475
QY 160 TAAAGTTGACAGGGCAATTCACCATTTATATTTTGGCGTGCATTGAATTGTTGGCATTTTCC 219
DB 474 TCACAGCTTTGGACATTTGTCGTTTATGCTGCGGTACATAGTATCCCATGCGAGTTTC- 416
QY 220 CTCCACTTGGATTAGTCGGGGCGAAAGTCATCGGTATATATAATCCATCAACTAAAGAAA 279
DB 415 -----GAACTAGTTGGGCTAAATCTCATAGGTATGTTAAATCCATCGACAAGTGAGA 364
QY 280 TGTCCAGAAATCTAAGTTGTTGAACTGGTCCAAAGGGTACTCGGCTAGGGTGTGTTGGTG 339
DB 363 TATCGTAGAAGTCTAAGTTGTTGAAATTTGGTTCAAGCGGTAATCAGCAACGTTGTTGGTG 304
QY 340 GTTTGCCCCCACCOCGGTGCATCGCAGGACACCAACCAATCACCAGTCTATGTCACGAACTTC 399
DB 303 GCTGTCCCCCGCCAGTACATTGGAGTCCACCACTCGAGTCCACAGTTTGGCATCGGCCAC 244
QY 400 TACCAGCACCATCGAAGTTTACATCCAGTACGAGCCCATATACCTGCGATCGTAGTGCCTCC 459
DB 243 GACCTGAGGAGTCAAAAGTTTACAAATTTGGTCTCTACCCCAAAATCCGTGCCATTTTGTAGT 184
QY 460 TAGGCGCATCAATGACCCCAATTTGCCCCCGATCGAAAGCTCGGACCCCGCTTTCGGGGT 519
DB 183 CCGCAGCATCTAGCTCCATGATTTGGCCAGCATCTAGAGTCCG--CCACCTCCAGGGCT 126
QY 520 CGATCGCCGCCAAACGATGATGAGCAGTTGTTGGTACCTCGATAGTGGCAGCATAAGT 579
DB 125 TCGCGCAGCCACACGGTGTAACTACATTTAGGTTTTCGAATGTTGGCGGCTGTTGTC 66
QY 580 GAAAGTCAAAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 625
DB 65 GGTGGAGATGACCAAAAGTGGCGGAAATATATGAAGTAGAGACCAAG 20

Search completed: August 18, 2004, 07:59:05
Job time : 578.148 secs

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 06:27:01 ; Search time 122.848 Seconds
(without alignments)
7205.239 Million cell updates/sec

Title: US-10-051-307-1
Perfect score: 1595
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	479.2	30.0	3033	1 US-08-482-037A-1	Sequence 1, Appli
C 2	430.2	27.0	883	1 US-07-828-798C-4	Sequence 4, Appli
C 3	430.2	27.0	883	2 US-08-315-868A-4	Sequence 4, Appli
C 4	430.2	27.0	883	3 US-08-495-819B-4	Sequence 4, Appli
C 5	430.2	27.0	884	1 US-07-828-798C-5	Sequence 5, Appli
C 6	430.2	27.0	884	2 US-08-315-868A-5	Sequence 5, Appli
C 7	430.2	27.0	884	3 US-08-495-819B-5	Sequence 5, Appli
C 8	170.4	10.7	875	4 US-09-589-733C-4	Sequence 4, Appli
C 9	155.2	9.7	900	1 US-08-181-271A-4	Sequence 4, Appli
C 10	155.2	9.7	900	1 US-08-449-315-4	Sequence 4, Appli
C 11	155.2	9.7	900	1 US-08-444-803-4	Sequence 4, Appli
C 12	155.2	9.7	900	1 US-08-449-043-4	Sequence 4, Appli
C 13	155.2	9.7	900	1 US-08-456-265A-4	Sequence 4, Appli
C 14	155.2	9.7	900	1 US-08-455-416-4	Sequence 4, Appli
C 15	155.2	9.7	900	1 US-08-455-244-4	Sequence 4, Appli
C 16	155.2	9.7	900	1 US-08-454-876-4	Sequence 4, Appli
C 17	155.2	9.7	900	1 US-08-457-364-4	Sequence 4, Appli
C 18	155.2	9.7	900	2 US-08-456-262-4	Sequence 4, Appli
C 19	155.2	9.7	900	2 US-08-456-240-4	Sequence 4, Appli
C 20	155.2	9.7	900	2 US-08-455-736-4	Sequence 4, Appli
C 21	155.2	9.7	900	2 US-08-971-217-4	Sequence 4, Appli
C 22	155.2	9.7	900	3 US-09-350-600-4	Sequence 4, Appli
C 23	155.2	9.7	900	4 US-09-906-234-4	Sequence 4, Appli
C 24	149	9.3	910	4 US-08-685-232-1	Sequence 4, Appli
C 25	106.4	6.7	894	1 US-08-178-708-7	Sequence 7, Appli
C 26	106.4	6.7	894	1 US-08-457-552-7	Sequence 7, Appli
C 27	106.4	6.7	894	1 US-08-456-430-7	Sequence 7, Appli

Query Match 30.0%; Score 479.2; DB 1; Length 3033;

ALIGNMENTS

RESULT 1

US-08-482-037A-1/c
; Sequence 1, Application US/08482037A
; Patent No. 5801028
; GENERAL INFORMATION:
; APPLICANT: Ray Bressan and Paul M. Hasegawa
; TITLE OF INVENTION: Osmotin Gene Promoter and Use Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas Q. Henry
; STREET: Bank One Tower, Suite 3700, 111 Monument Circle
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204-5137
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: COMPAQ
; OPERATING SYSTEM: MSDOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,037A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,243
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/180,428
; FILING DATE: January 12, 1994
; APPLICATION NUMBER: 08/065,147
; FILING DATE: May 20, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas Q. Henry
; REGISTRATION NUMBER: 28,309
; REFERENCE/DOCKET NUMBER: 7024-8/PUR16ICPDIVII
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 634-3456
; TELEFAX: (317) 637-7561
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 bases
; TYPE: Nucleotide/Amino Acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: Genomic DNA
; US-08-482-037A-1

C 28	106.4	6.7	894	2	US-08-994-418-7	Sequence 7, Appli
C 29	106.4	6.7	894	5	PCI-US95-00432-7	Sequence 7, Appli
C 30	97.4	6.1	1309	6	5221624-4	Patent No. 5221624
C 31	90.6	5.7	621	4	US-09-224-514A-1	Sequence 1, Appli
C 32	90.6	5.7	621	6	5221624-31	Patent No. 5221624
C 33	89	5.6	621	4	US-09-224-514A-9	Sequence 9, Appli
C 34	86.2	5.4	624	2	US-08-426-599B-3	Sequence 3, Appli
C 35	78.4	4.9	624	2	US-08-426-599B-1	Sequence 1, Appli
C 36	73.2	4.6	2051	1	US-08-482-037A-2	Sequence 28, Appli
C 37	64.6	4.1	230	4	US-09-589-733C-28	Sequence 1, Appli
C 38	60.8	3.8	640681	4	US-09-790-988-1	Patent No. 5231168
C 39	59	3.7	3095	6	5231168-1	Sequence 5, Appli
C 40	52.2	3.3	1924	4	US-09-424-283-5	Sequence 14, Appli
C 41	52	3.3	6113	4	US-10-204-708-14	Sequence 38, Appli
C 42	49.8	3.1	288	4	US-09-598-401C-38	Sequence 1, Appli
C 43	49.6	3.1	6152	3	US-08-973-462-1	Sequence 25, Appli
C 44	49.6	3.1	6593	4	US-10-204-708-25	Sequence 13, Appli
C 45	49	3.1	19124	2	US-08-487-826B-13	

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Best Local Similarity 76.9%; Pred No. 1.2e-101;
Matches 678; Conservative 0; Mismatches 163; Indels 41; Gaps 6;
QY 46 GGTATCTTTGTTGAAATTTGAAAGAAAGCTGAGGACACATGACCTTGGTGCAC 105
Db 2622 GGCATCTTTGTTGAAATTTGAGAAAAATGTAGGACACAGGTCCTTGTGTGCA 2563
QY 106 AATATTGTTGCTCCCAATTTGTGTACAAGATTTGATCTCCCGGTACTTTAAGT 165
Db 2562 AATATTGTTGCTCCCAATTTGTGTACAAGATTTGATCTCCCGGTACTTTAAGT 2503
QY 166 GACGAGGCAATTCACCAATTTATATTGCTGCAATGAATTTGTGTCATTTCCCTCC 225
Db 2502 CGCGGGGACATTCGCGCTTTATATTAGCGTACAAATGAATTCATGTCCTCCAC 2443
QY 226 TTGATTTAGTGGGGGCAAGTCTCGGTATATTAATTCATCACTAAAGAATGTCC 285
Db 2442 TAGGGTTAGTGGGGGCAAGTCTCGGTATATTAATTCATCACTAAAGAATGTCC 2383
QY 286 AGAATCTAAGTTGTTGAATCTGGTCCCAAGGCTACTCGGTAGGTTGTTGGTGGTTC 345
Db 2382 AGAATCTAAGTTGTTGAATCTGGTCCCAAGGCTACTCGGTAGGTTGTTGGTGGTTC 2323
QY 346 CCCACCGGTGCACTGAGGACACCAACCAATCAGTCATGTCAGAACTCTTACCAG 405
Db 2322 CCCACCGGTGCACTGAGGACACCAACCAATCAGTCATGTCAGAACTCTTACCAG 2263
QY 406 CACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCTAGTCCCTAGGG 465
Db 2362 CAGCATTAAGTTAATTTAGTACGCGCCCATCATACGTCGCATTTAGTACCTCTGG 2203
QY 466 CATCAATGACCCCAATTTGGCCCGCATGCAAGCTGG-CACCGCTTTCCGGGTCCAGT 524
Db 2202 CATTTGATCACCAGTTTGGCTCTGATCGAGAGCGCGGCCACCGCTATGGGTGCGAG 2143
QY 525 CCGCCCAACGATGTATGGACAGTTGTTGCTAGTCTGATAGTGGGCGCATAGTGAAG 584
Db 2142 CCGCCCAACGATGTATGGACAGTTGTTGCTAGTCTGATAGTGGGCGCATAGTGAAG 2083
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Db 2082 TCACAAAGCAAGAGGAGAGAAACAAAGAAAGATCTCAAGTAGCCCATGTTTGTGACA 2023
QY 645 TTTATATGTGACAAATTTATTTTGGTACT-----TTATATATAGG 685
Db 2022 TTTTATTAACAGTTGGTTGTTGGTATAGTACAAATTTTGTAGTGGTTTATATAGG 1963
QY 686 GATATGGCGCTTTTGGCACTACGATATTAATCGTATTTATATAGCAATATCATACTTTG 745
Db 1962 GGAATGGCGCTTTTGGCACTACGATATTAATCGTATTTATATAGCAATATCATACTTTG 1908
QY 746 ACTAATTATAACGAAATATATTAATTAATTAATTTGTTGTAACGTTGAGGTGG-AAAAATG 804
Db 1907 ACTA---ATRAACGGATATATCTCAAGGATGCTTTGGCAAGATGAGGCGGGCTTAA 1851
QY 805 TATAGAGCGCTTAATTAATTAATTTATTTATGATATAGCTATAGTACAAAGTTAACT 864
Db 1850 CATAGAGCGCTTAATTAATTAATTTATTTATGATATAG-----AAGTCAAT 1803
QY 865 TTATTTGTTGATATCTTTGACATATAAATCTCTGTAACGTGAC 906
Db 1802 TTATTTGTTGATATCTTTGACATATAAATCTCTGTAACGTGAC 1761

```

RESULT 2
 US-07-828-798C-4/c
 ; Sequence 4, Application US/07828798C
 ; Patent No. 5389609
 ; GENERAL INFORMATION:
 ; APPLICANT: Woloshuk, Charles P.
 ; APPLICANT: Melchers, Leo S.
 ; APPLICANT: Cornelissen, Bernardus J. C.
 ; APPLICANT: Meulenhoff, Elisabeth J. S.

```

; APPLICANT: Sela-Buurlage, Marianne B.  

; APPLICANT: Van Den Elzen, Petrus J. M.  

; TITLE OF INVENTION: Antifungal Preparations, Process for  

; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with  

; TITLE OF INVENTION: Decreased Susceptibility to Fungi  

; NUMBER OF SEQUENCES: 7  

; CORRESPONDENCE ADDRESS:  

; ADDRESSEE: Ladas & Parry  

; STREET: 26 West 61st Street  

; CITY: New York  

; STATE: New York  

; COUNTRY: USA  

; ZIP: 10023  

; COMPUTER READABLE FORM:  

; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  

; COMPUTER: IBM PC/XT/AT or compatibles  

; OPERATING SYSTEM: DOS  

; SOFTWARE: Word Perfect 5.1  

; CURRENT APPLICATION DATA:  

; APPLICATION NUMBER: US/07/828,798C  

; FILING DATE: 06-APR-1992  

; CLASSIFICATION: 514  

; PRIOR APPLICATION DATA:  

; APPLICATION NUMBER: PCT/NL91/00089  

; FILING DATE: 31-05-91  

; ATTORNEY/AGENT INFORMATION:  

; NAME: Mass, Clifford J.  

; REGISTRATION NUMBER: 30086  

; REFERENCE/DOCKET NUMBER: U-8622-6  

; TELECOMMUNICATION INFORMATION:  

; TELEPHONE: (212) 708-1800  

; TELEFAX: (212) 246-8959  

; INFORMATION FOR SEQ ID NO: 4:  

; SEQUENCE CHARACTERISTICS:  

; LENGTH: 883  

; TYPE: Nucleotide  

; STRANDEDNESS: Double  

; TOPOLOGY: Linear  

; MOLECULE TYPE: cDNA  

; ORIGINAL SOURCE:  

; ORGANISM: Nicotiana tabacum  

; US-07-828-798C-4

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Query Match 27.0%; Score 430.2; DB 1; Length 883;
Best Local Similarity 84.1%; Pred. No. 1.8e-90;
Matches 497; Conservative 0; Mismatches 93; Indels 1; Gaps 1;
QY 46 GGTATCTTTGTTGAAATTTGAAAGAAAGCTGAGGACACATGACCTTGGTGCAC 105
Db 605 GGCATCTTTGTTGAAATTTTGAATAATTTGAGAAATTTAGGACCAAGTCTTGTGCAAC 546
QY 106 AATATTGTTGCTCCCAATTTGTGTACAAGATTTGTATCATCTCCGGGTACTTTAAGT 165
Db 545 AATATTGTTGCTCCCAATTTGTGTACAAGATTTGTATCATCTCCGGGAAACCTTAAGT 486
QY 166 GACGAGGCAATTCACCAATTTATTTGCGGTGCAATTTGAATTTGTGTCATTTCCCTCCAC 225
Db 485 CGCGGGGCAATTCGCGCTTTATTTAGCCGTACAAATGAATTCATGTCATTTCCCTCCAC 426
QY 226 TTGATTTAGTGGGGGCAAGTCTCGGTATATTAATTCATCACTAAAGAATGTCCC 285
Db 425 TAGGGTTAGTGGGGGCAAGTCTCGGTATATTTAGCCGTACAAATGAATTCATCACTAAAGAATGTCCC 366
QY 286 AGAATCTAAGTTGTTGAATCTGGTCCCAAGGCTACTCGGTAGGTTGTTGGTGGTTC 345
Db 365 AGAATCTAAGTTGTTGAATCTGGTCCCAAGGCTACTCGGTAGGTTGTTGGTGGTTC 306
QY 346 CCCACCGGTGCACTGAGGACACCAACCAATCAGTCATGTCAGAACTCTTACCAG 405
Db 305 CCCACCGGTGCACTGAGGACACCAACCAATCAGTCATGTCAGAACTCTTACCAG 246
QY 406 CACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCTAGTGGCGCTTACCAG 465

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245	CAGCATTGAGTTACAAATTAGTAGCGGCCCATACAGTGCATTTTAGTACCTCTGTGGCG	186
466	CATCAATGACCCACATTTTGGCCCCGATCGAAAAGTGG - CACCCGTTTTGGGGTTCGATG	524
185	CATTGATCACCCAAAGTTTGGCTCGATCGAGACGCCGCCACCGCTTAGGGTGTGCGAG	126
525	CGGCCCAAACGATGTATCGACAGTTTGTTCGTACTCGATAGTGGCAGCATAGTCAAG	584
125	CGGCCCAAACGGTGTACGACAGTTGTTTCGACCTCGATAGTGGCAGCATAGTATNAG	66
585	TCACAAAGCAAGAGGGAGAAAACAAAGAGATCTCAAGTAGCCCATGT	635
65	TCACCAAGGCAAGAGGAAGAAAACAAAGAGATCTCAAGTTGCCCATGT	15

RESULT 3

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US-08-315-868A-4/c
; Sequence 4, Application US/08315868A
; Patent No. 5856151
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marijanne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi

```

NUMBER OF SEQUENCES: 7

```

CORRESPONDENCE ADDRESS:
ADDRESSER: Ladas & Parry
STREET: 26 West 61st Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PC/XT/AT or compatibles
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315.868A
FILING DATE: 09-SEP-1994
CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/828,798
 ; FILING DATE: 06-APR-1992
 ; APPLICATION NUMBER: PCT/NL91/00089
 ; FILING DATE: 31-05-91
 ; ATTORNEY/AGENT INFORMATION:
 ;

NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30086
REFERENCE/DOCKET NUMBER: U-8622-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
TELEFAX: (212) 246-8959
TELEX: 233288

; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 883

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; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
US-08-315-869A-4

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Query Match 27.0%; Score 430.2; DB 2; Length 883;
Best Local Similarity 84.1%; Pred. No. 1.8e-90;

	Matches	497;	Conservative	0;	Mismatches	93;	Indels	1;	Gaps	1;
QY	46	GGTATCTTTGTTTGGAAAAAATTTGGAAAAAGAAAGCTAGGACACATAGACCTTGGGTGCAAC	105							
Db	605	GGCATCTTTGTTTGGAAAAAATTTTGAAAAAATGTAGGACCAAAAGGTCCTTGTGTGCAAC	546							
QY	106	AATATGTTGTCTCCTCCAAATGCGTCAAGGATGTTATCATCTCTCGGGTACTTTAAGTT	165							
Db	545	AATATGTTGTCTCCTCGAATGAGTACAAGGGTTATTATCTCTCGGGAACCTAAGTT	486							
QY	166	GACCAAGGCATTCACCATTTATTTGCGGTGCATTGAATTTGTGTGGCATTTCCCTCCAC	225							
Db	485	CGCGGGACATTCGCGGTTTATTATAGCCGTACAATGAATGCATGCATTTCCCTCCAC	426							
QY	226	TTTGGATTTAGTCGGGGGAAAGTCATCGGTATATTAATCCATCAATAAAGAAATGTCCC	285							
Db	425	TAGGGTTTAGTCGGGGCGAAAGTCATCGGAATGTGAATCCATCAACTAAAGAAATGTCCC	366							
QY	286	AGAAATCTAAGTTGTTTGAACCTCGTCCAAAGCGGTACTCGGCTAGGGTGTGTGGTGGTTGC	345							
Db	365	AGAAATCTAAACCACTGAATTTGGTCCAAAGCGGTATTCAGCAAGGTGTTTGGTGGTTTAC	306							
QY	346	CCACCCGGTGCACCTGCAGGACACCAACAATCACCACTCATGCACGAACCTCTACCAG	405							
Db	305	CCACCCGGTGCACGTAGGACTCCACCAACAGTCACCGGTGGGCAGTACCCCTACCAG	246							
QY	406	CAACATCGAAGTTACATCCAGTAGACGCCCATATACCTGCCATCTGTAGTGCCCTTAGCG	465							
Db	245	CAGCATTTGAAGTTACAAATTTAGTACGGCGCCCATACAGTGCCTTTTAGTACCTCTGGCG	186							
QY	466	CATCAATGACCCACATTTGCGCCCGATCGAAAGTCTGG-CACCCGCTTTCGGGGTCCGATG	524							
Db	185	CATTGATCAACCAAGTTTGGCTTCGATCGAGACCGCGGCCACCGCTATGGGTGTCTGACG	126							
QY	525	CGGCCCAACGATGTATGACACAGTTGTTGCGTACCTTCGATAGTGGCAGCATATAAGTGAAG	584							
Db	125	CGGCCCAACCGGTGTACGCACAGTTGTTTCGGACCTCGATAGTGGCAGCATATAGTATAAG	66							
QY	585	TCACAAAACAGAGGGGAGAAAAAAGAGATCTCAAGTAGCCCATGT	635							
Db	65	TCACCAAGCCAAAGGAGGAGAAAAAAGAGAGATCTCAAGTTGCCCATGT	15							

RESULT 4

US-08-495-819B-4/C
 / Sequence 4, Application US/08495819B
 / Patent No. 6087161
 / GENERAL INFORMATION:
 / APPLICANT: Woloshuk, Charles P.
 / APPLICANT: Melchers, Leo S.
 / APPLICANT: Cornelissen, Bernardus J. C.
 / APPLICANT: Meulenhoff, Elisabeth J. S.
 / APPLICANT: Sela-Buurlage, Marianne B.
 / APPLICANT: Van Den Elzen, Petrus J. M.
 / TITLE OF INVENTION: Antifungal Preparations, Process for
 / TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants
 / TITLE OF INVENTION: with Decreased Susceptibility to Fungi
 / NUMBER OF SEQUENCES: 7
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Ladas & Parry
 / STREET: 26 West 61st Street
 / CITY: New York
 / STATE: New York
 / COUNTRY: USA
 / ZIP: 10023
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
 / COMPUTER: IBM PC/XT/AT or compatibles
 / OPERATING SYSTEM: DOS
 / SOFTWARE: Word Perfect 5.1
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/495.819B
 / FILING DATE: 31-MAY-1995

QY 286 AGAATCTAAGTTGTTGAACCTGGTCCAAAGGCGTACTCGGCTAGGGTGTGGTGGTTGC 345
Db |||||||
QY 365 AGAATCTAAGTTGTTGAACCTGGTCCAAAGGCGTACTCGGCTAGGGTGTGGTGGTTAC 306
Db |||||||
QY 346 CCCACCCCGTGCACCTGACGAGGACACCAACACCAATACCAAGTATCGACGAACTCTACAG 405
Db |||||||
QY 305 CCCACCCCGTGCACCTGACGAGGACACCAACACCAATACCAAGTATCGACGAACTCTACAG 246
Db |||||||
QY 406 CACATCGAAGTTACATCCAGTACGACCCCATATACCTGATCGATCGATCGATCGATCGATCG 465
Db |||||||
QY 245 CAGCATTAAGTTTAAATAGTACGACCCCATATACCTGATCGATCGATCGATCGATCGATCG 186
Db |||||||
QY 466 CATCAATGACCCACATTTGGCCCGATCGAAAGCTCGG-CACCCGCTTTCGGGTCGATG 524
Db |||||||
QY 185 CATGATCACCACCAAGTTTGGCCCTGATCGACGCGCGCCACCCCTATGGGTGTCGACG 126
Db |||||||
QY 525 CGGCCAAACAGTATGATGACGAGTTGTTGCGTACTCGATAGTGGCAGCATAACTGAAAG 584
Db |||||||
QY 125 CGGCCAAACAGTATGATGACGAGTTGTTGCGTACTCGATAGTGGCAGCATAACTGAAAG 66
Db |||||||
QY 585 TCACAAAGCAAGGAGGAGAAACAAAGAAAGATCTCAAGTACCCCATGT 635
Db |||||||
QY 65 TCACAAAGCAAGGAGGAGAAACAAAGAAAGATCTCAAGTACCCCATGT 15
Db |||||||

RESULT 6
US-08-315-868A-5/c
; Sequence 5, Application US/08315868A
; Patent No. 5856151
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08315,868A
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APR-1992
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-8622-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884

TYPE: Nucleotide
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Nicotiana tabacum
US-08-315-868A-5
Query Match 27.0%; Score 430.2; DB 2; Length 884;
Best Local Similarity 84.1%; Pred. No. 1.8e-90;
Matches 497; Conservative 0; Mismatches 93; Indels 1; Gaps 1;
QY 46 GGTATCTTTGTTGAAAAAATTGGAAAAAGAAAGTAGGACACATGACCTTGGGTGCAAC 105
Db |||||||
QY 605 GGCATCTTTGTTGAAAAAATTGGAAAAAATGTTAGAACCAAGGTCTTGTGTGCAAC 546
Db |||||||
QY 106 AATATTGTTGTCCTCCAAATGTTGTAACAAGGATTTTACATCTCCGGGTACTTTAAGTT 165
Db |||||||
QY 545 AATATTGTTGTCCTCCGAATGTTAGTACAAGGTTATTACATCTCCGGGAAACCTTAAGTT 486
Db |||||||
QY 166 GACCAGGGATTCACCATTTATATTGTCCTGATGATTAAGTTGTTGGCATTTCCCTCCAC 225
Db |||||||
QY 485 CGCGGGGACATTTGCGCGTTTATATTAGCGGTACAATGAATTCATGGCATTTCCCTCCAC 426
Db |||||||
QY 226 TTGGATTAGTCGGGGGCAAGTATCGGTATATTAAATCCATCAACTAAAGAAATGTCCTC 285
Db |||||||
QY 425 TAGGTTAGTCGGGGGCAAGTATCGGTATATTAAATCCATCAACTAAAGAAATGTCCTC 366
Db |||||||
QY 286 AGAATCTAAGTTGTTGAACTGGTCCAAAGCGTACTCGGCTAGGGTGTGGTGGTTGC 345
Db |||||||
QY 365 AGAATCTAAGTTGTTGAACTGGTCCAAAGCGTACTCGGCTAGGGTGTGGTGGTTGC 306
Db |||||||
QY 346 CCACCCCGTGCACCTGACGAGGACACCAACATCAAGTATCGGCTAGGGTGTGGTGGTTGC 405
Db |||||||
QY 305 CCACCCCGTGCACCTGACGAGGACACCAACATCAAGTATCGGCTAGGGTGTGGTGGTTGC 246
Db |||||||
QY 406 CACCATCGAAGTTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTCCCTAGGGG 465
Db |||||||
QY 245 CAGCATTAAGTTTACATTAAGTTAGTACGCGCCCATACAGTGCCATTTAGTACCTCGTGGG 186
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QY 466 CATCAATGACCCACATTTGGCCCGATCGAAAGCTCGG-CACCCGCTTTCGGGTCGATG 524
Db |||||||
QY 185 CATGATCACCACCAAGTTTGGCCCTGATCGACGCGCGCCACCCCTATGGGTGTCGACG 126
Db |||||||
QY 525 CGGCCAAACAGTATGATGACGAGTTGTTGCGTACTCGATAGTGGCAGCATAACTGAAAG 584
Db |||||||
QY 125 CGGCCAAACAGTATGATGACGAGTTGTTGCGTACTCGATAGTGGCAGCATAACTGAAAG 66
Db |||||||
QY 585 TCACAAAGCAAGGAGGAGAAACAAAGAAAGATCTCAAGTACCCCATGT 635
Db |||||||
QY 65 TCACAAAGCAAGGAGGAGAAACAAAGAAAGATCTCAAGTACCCCATGT 15
Db |||||||

RESULT 7
US-08-495-819B-5/c
; Sequence 5, Application US/08495819B
; Patent No. 6087161
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants
; TITLE OF INVENTION: with Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York

QY 529 CCAACGATGTATGACAGTGTTCGCTACCTCGATAGTGGCAGCATAGTGAAGTCAAC 588
 Db |||||
 105 CCAACGGTGTATGACAGTGTTCGCTACCTCGATAGTGGCAGCATAGTGAAGTCAAC 46
 QY 589 AAAA 592
 Db |||||
 45 AAGA 42

RESULT 9

US-08-181-271A-4/C
 ; Sequence 4, Application US/08181271A
 ; Patent No. 5614395
 ; GENERAL INFORMATION:
 ; APPLICANT: Ryals, John A.
 ; APPLICANT: Alexander, Danny C.
 ; APPLICANT: Beck, James J.
 ; APPLICANT: Duesing, John H.
 ; APPLICANT: Friedrich, Leslie B.
 ; APPLICANT: Goodman, Robert M.
 ; APPLICANT: Harms, Christian
 ; APPLICANT: Meins, Jr., Frederick
 ; APPLICANT: Montoya, Alice
 ; APPLICANT: Moyer, Mary B.
 ; APPLICANT: Neuhaus, Jean-Marc
 ; APPLICANT: Payne, George B.
 ; APPLICANT: Sperison, Christoph
 ; APPLICANT: Stinson, Jeffrey R.
 ; APPLICANT: Uknes, Scott J.
 ; APPLICANT: Ward, Eric R.
 ; APPLICANT: Williams, Shericca C.
 ; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 ; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CIBA-GEIGY Corporation
 ; STREET: 7 Skyline Drive
 ; CITY: Hawthorne
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10532
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/181,271A
 ; FILING DATE: 13-JAN-94
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/093,301
 ; FILING DATE: 16-JUL-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/937,197
 ; FILING DATE: 6-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/578,378
 ; FILING DATE: 1-APR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/305,566
 ; FILING DATE: 6-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/165,667
 ; FILING DATE: 8-MAR-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/042,847
 ; FILING DATE: 6-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/632,441
 ; FILING DATE: 21-DEC-1990
 ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/425,504
 ; FILING DATE: 20-OCT-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/848,506
 ; FILING DATE: 6-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/768,122
 ; FILING DATE: 27-SEP-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/580,431
 ; FILING DATE: 7-SEP-1990
 ; APPLICATION NUMBER: US 07/368,672
 ; FILING DATE: 20-JUN-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/329,018
 ; FILING DATE: 24-MAR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/045,957
 ; FILING DATE: 12-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Elmer, James Scott
 ; REGISTRATION NUMBER: 36,129
 ; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919)541-8614
 ; TELEFAX: (919)541-8689
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 900 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-181-271A-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;

Best Local Similarity 60.5%; Pred. No. 7.4e-27;

Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;

QY 46 GGTATCTTTGTTTGAAGAAATTCGAAAGACGTAGGACACAT-----GGACCTTGGG 99
 Db |||||
 607 GGCATCTTTCTTAAATAATCTCGACAATCAGTAGGCCACATGATCCAGGCCCATTTG 548
 QY 100 TGCACAATATTGTTCTCTCCAAATGTGTGTACAGGATTTACATCTCCGGGTACTTT 159
 Db |||||
 547 TACAACATATTCAITGGTTTTTATCACAGTACATGGGTGTTTACATCCACCTTGTGTTT 488
 QY 160 TAAGTTGACGAGGCAATCCACATTTATATTTGCGGTGCATTTGAATTGTGTCATTTCC 219
 Db |||||
 487 TCACGTGCTGGCAATTTGTTGTTAATAGGTGCTGTGCATCTGAGATTACACAT---- 432
 QY 220 CTCCACTTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAATCAATCAACTAAAGAAA 279
 Db |||||
 431 -----CTCCATTTGGTGGGCTGAATTCATGGGATGTTAAATCCATCAACAAGAGA 377
 QY 280 TGTCCAGAAATCTAAGTTGTTGAATCGTCAAGGCGTACTCGGCTAGGGTGTGGTG 339
 Db |||||
 376 TGTGCAAAAGTC---CTGATTGGGTGATTAAAGTCAAAATTCAGCTAAAGTGTAGGTG 320
 QY 340 GTTTGCCCCACCCGGTGCATCTCAGGACACCAACCAATCACCAGTCTATGCACGACCTC 399
 Db |||||
 319 CTTTTCATAGCTTTGACACTTAACATCCCGTTACAGTCTCCAGTCTCACAATTACCTC 260
 QY 400 TACCAGCACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTGCCTC 459
 Db |||||
 259 GGCCACTGCCATCGAAGTTGCAATTGGTTTCGACCCCAATTCGAGCCTTGCCTTCCTG 200
 QY 460 TAGGGGCATCAATGACCCACATTTTGGCCCGGATCGAAACGTCGGACCCCGCTTCGGGGT 519
 Db |||||
 199 GGTTCACATTAATGCTCCAGATTGGCTGAGTCCAGCGGCTGCTCCACCT--GGAGA 142
 QY 520 CGATCGCGCCCAACGATGTATGGACAGTTGTTGGTACCTCGATAGTGGCAGCATAAGT 579

Db 141 GCGCGCGCCAGACTGTGTAGTGTGCTTTGTTGACAATGTCAAAAGTGGCAGCATGAGT 82

Qy 580 GAAAGTCACAAA 591

Db 81 AACAGCTACAAA 70

RESULT 10

US-08-449-315-4/c

; Sequence 4, Application US/08449315

; Patent No. 5650505

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Melms, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Scinson, Jeffrey R.

; APPLICANT: Ukes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,315

; FILING DATE: 24-MAY-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/181,271

; FILING DATE: 13-JAN-94

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,197

; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/678,378

; FILING DATE: 1-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/042,847

; FILING DATE: 6-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/632,441

; FILING DATE: 21-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/425,504

; FILING DATE: 20-OCT-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/848,506

; FILING DATE: 6-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/768,122

; FILING DATE: 27-SEP-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/580,431

; FILING DATE: 7-SEP-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/368,672

; FILING DATE: 20-JUN-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/329,018

; FILING DATE: 24-MAR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/045,957

; FILING DATE: 12-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Elmer, James Scott

; REGISTRATION NUMBER: 36,129

; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8614

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 900 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-449-315-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;

Best Local Similarity 60.5%; Pred. No. 7.4e-27;

Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;

Qy 46 GGTATCTTTGTTGAAAAAATTGGAAAAAGACGTAGGACCCACAT-----CGACCTTGGG 99

Db 607 GCATCTTTCTTAAAAAATCTCGACAAATCAGTAGGCCACATGATCCAGGCCCATTTG 548

Qy 100 TGCAACAATATTTGTCTCTCCAAATGTGGTACAGGATTTGTATCATCTCTCGGGTACTT 159

Db 547 TACAACAATATTCATTGGTTTTTTATTCACAGTACATGGGTTGTATCATCCACCTTGTGTT 488

Qy 160 TAAAGTTGACAGGCAATTCACATTTATTTGCGTGCATTGAATTTGTGTGGCATTTCC 219

Db 487 TCAACTGTCTGGGCATTGTCGTTAATAGTGTCTGTGCACTGAGATTAGACAT----- 432

Qy 220 CTCACACTTGGATTAGTCGGGGCGAAAGTCATCGGTATATAAATCCATCAACTAAAGAAA 279

Db 431 -----CCTCCATTGTCGGCTGGAATTCATGGGGATGTTAAATCCATCAACAAGAGAGA 377

Qy 280 TGTCCAGAAATCTAAGTTGTTGAATCTGTCAGGCGTACTCGCTAGGGTGTGGTG 339

Db 376 TGTGACAAAGTTC---CTGATTTGGGTTGATTAAAGTGAATTCAGCTAAAGTGTAGGTG 320

Qy 340 GTTTGCCCCACCCGGTGCACCTGCAGGACACCAACAATCCACAGTCATGACGAAACCTC 399

Db 319 CTTTTCCATAGCCTTGACACTTAACATCCCGTTACAGTCTCCAGTCTCACATTAACCTC 260

Qy 400 TACCAGCACCATCGAAGTTAATCATCAGTACAGCCCATATACCTGCCATCTAGTAGCCCC 459

Db 259 GGCCCACTGCCATCGAAGTTGCAATTTGTTTCGACCCCAAAATCGAGCCTTGGACTGTCTG 200

Qy 460 TAGGGCGCATCATGACCCACATTTTGGCCCCCGATTCGAAACGTCGGCACCCGCTTCGGGGT 519

Db 199 GGTTCACATTAATGCTCCAGATTGGCTGAGTGGAGCCGCTGCTCCACCT--GGAGA 142

Qy 520 CGATGCCGCCCAACCATGATGTATGGACAGTTGTGTGCTACCTCGATAGTGGCAGCATAAAGT 579

Db 141 GCGCGGCGCCAGATGTGTAGTGCATTTGTTGCAATGTCAAAAGTGGCAGCATGAGT 82
 QY 580 GAAAGTCACAA 591
 Db 81 AACAGCTACAA 70

RESULT 11
 US-08-444-803-4/c
 ; Sequence 4, Application US/08444803
 ; Patent No. 5654114
 ; GENERAL INFORMATION:
 ; APPLICANT: Ryals, John A.
 ; APPLICANT: Alexander, Danny C.
 ; APPLICANT: Beck, James J.
 ; APPLICANT: Duesing, John H.
 ; APPLICANT: Friedrich, Leslie B.
 ; APPLICANT: Goodman, Robert M.
 ; APPLICANT: Harms, Christian
 ; APPLICANT: Meins, Jr., Frederick
 ; APPLICANT: Montoya, Alice
 ; APPLICANT: Moyer, Mary B.
 ; APPLICANT: Neuhaus, Jean-Marc
 ; APPLICANT: Payne, George B.
 ; APPLICANT: Sperison, Christoph
 ; APPLICANT: Stinson, Jeffrey R.
 ; APPLICANT: Uknes, Scott J.
 ; APPLICANT: Ward, Eric R.
 ; APPLICANT: Williams, Shericca C.
 ; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 ; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CIBA-GEIGY Corporation
 ; STREET: 7 Skyline Drive
 ; CITY: Hawthorne
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10532

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,803
 ; FILING DATE: 19-MAY-1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/181,271
 ; FILING DATE: 13-JAN-94
 ; APPLICATION NUMBER: US 08/093,301
 ; FILING DATE: 16-JUL-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/937,197
 ; FILING DATE: 6-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/678,378
 ; FILING DATE: 1-APR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/305,566
 ; FILING DATE: 6-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/165,667
 ; FILING DATE: 8-MAR-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/042,847
 ; FILING DATE: 6-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/632,441
 ; FILING DATE: 21-DEC-1990
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT 1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 900 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-444-803-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;
 Best Local Similarity 60.5%; Pred. No. 7.4e-27;
 Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;

QY 46 GGTATCTTTGTTGAAAAAATGGAAAAAGAGTAGGACCACAT-----GGACCTTGGG 99
 Db 607 GGATCTTTTCTTAAATAATCTGCACAAATCATAGTAGGCCACATATCCAGGCCCATTTG 548
 QY 100 TGCAACAATATTGTTGCTCTCCAAATGTGTTACAGGATTGTACATCTCCGGGTACTT 159
 Db 547 TACACAATATTCAATGTTGTTTTATCAGATACATGGTTGTATCATCCACCTTGTTT 488
 QY 160 TAAGTTGACAGGCAATCCCAATTTATTTGCGGTGCANTGAATTTGTGGCAATTTCC 219
 Db 487 TCAACTGTCTGGCAATTTGCTTAATAGGTGCTGTGCATCTGAGATTACGACAT---- 432
 QY 220 CTCCACTTGGATTAGTCGGGGGAAAGTCATCGGTATATTAATCCATCAACTAAGAA 279
 Db 431 -----CTCCATTTGGTCGGGCTGAATTCATGGGATGTTAAATCCATCAACAGAGA 377
 QY 280 TGTCCAGAAATCTAAGTTGTTGAACTGGTGTCAAGCGGTACTCGGCTAGGTTGTTGGTG 339
 Db 376 TGTGCACAAAGTC---CTGATTGGTGTGATTAAAGTGCAAATTCAGTAAAGTTAGGTG 320
 QY 340 GTTTGCCCCCAGCGGTGCACTGCAGGACACCAACCAATCACCAGTCATGCAGGACCTC 399
 Db 319 CTTTTCATAGCTTGACATCTAAATCCCGTTTACAGTCTCCAGTCTCACAATTAACCTC 260
 QY 400 TACCAGCACTCGAAGTTTACATCCAGTACGACCCCATATACCTGCGATCGTAGTGCCTC 459
 Db 259 GGCCACTGCAATCGAAGTTGCAATTTGTTGACCCCAATTCGAGCCTGGACTGTTCTCTG 200
 QY 460 TAGGGCATCATGATGACCCACATTTGGCCCCGATCAAAAGCTGGGACCGCTTTCCGGGT 519
 Db 199 GGTTCACATTAATGCTCCAAGATTGGCTGTAGTCGAGCGCGCTGCTCCACCT--GGAGA 142
 QY 520 CGATGCGGCCCAACAGATGTATGGACAGTTGTTGGTCTACCTCGATAGTGGCAGCATAGT 579

Db 141 GCGCGCGCCAGACTGTAGTGGTCAATTTGTCACATCTCAAAAGTGGCAGCATGACT 82

Qy 580 GAAAGTCACAAA 591

Db 81 AACAGTCAAAA 70

RESULT 12

US-08-449-043-4/c

; Sequence 4, Application US/08449043

; Patent No. 5689044

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,043

; FILING DATE: 24-MAY-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/181,271

; FILING DATE: 13-JAN-94

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/337,197

; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/678,378

; FILING DATE: 1-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/042,847

; FILING DATE: 6-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/632,441

; FILING DATE: 21-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/425,504

; FILING DATE: 20-OCT-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/848,506

; FILING DATE: 6-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/768,122

; FILING DATE: 27-SEP-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/580,431

; FILING DATE: 7-SEP-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/368,672

; FILING DATE: 20-JUN-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/329,018

; FILING DATE: 24-MAR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/045,957

; FILING DATE: 12-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Elmer, James Scott

; REGISTRATION NUMBER: 36,129

; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8614

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 900 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-449-043-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;

Best Local Similarity 60.5%; Pred. No. 7.4e-27;

Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;

Qy 46 GGTATCTTTTGTGAAAAAATGGAAAAAGACGTAGGACCAAT-----GGACCTTGGG 99

Db 607 GGCATCTTTTCTTAAAAAATCTCGACAAATCAGTAGGCCACATCATCCAGGCCCAATTG 548

Qy 100 TGCACAAATNTGTTGCTCTCCAAATGGTACAGGATTTGTATCATCTCCGGGTACTT 159

Db 547 TACAAATATTTTCATTTGTTTTTATCAGTACATGGGTTGTTATCATCCACTTGTGTTT 488

Qy 160 TAAAGTTGACCGGGCATTCACCAATTTATTTTGGCGTGCAATTTGATTTGGCAATTTCC 219

Db 487 TCAACTGTCTGGGCATTTGTTGTTAATAGTGCTGTGCACTGAGATTACGACAT----- 432

Qy 220 CTCCACTTTGGATTAGTCGGGGGGAAGTCATCGGTATATTAAATCCATCACTAAGAA 279

Db 431 -----CCTCCATTTGTCGGGCTGAATTCATGGGATTTAAATCCATCAACAGAGAGA 377

Qy 280 TGTCCAGAAATCTAAGTTGTTGAACTGGTCCAAGCGCTACTCGGCTAGGGTGTGTTGGTG 339

Db 376 TGTGCACAAAGTC---CTGATTTGGTTGATTAAGTGCAAAATTCAGTAAAGTTAGGTG 320

Qy 340 GTTTGCCCCACCCGGTGCACTGCAGGACACCAACCAATCACCAGTCATGCACGACCTC 399

Db 319 CTTTTCATAGCCTTGACACTTAACATCCCGTTACAGTCTCCAGTCTCAAAATTACCTC 260

Qy 400 TACCAGCACCATCGAAGTTTACATCCAGTACGACCCCATATACCTGCCATCTAGTGCCTCC 459

Db 259 GGCCACTGCCATCGAAGTTGCAATTTGGTTGCACCCCAATTCGAGCTGGACTGTTCTGTG 200

Qy 460 TAGGGCGCATCAATGACCCACATTTTGGCCCCGATTCGAAAGTCGCGGACCCGCTTTCGGGGT 519

Db 199 GGTTCACATTAATGCTCCAAAGATTGGCCTGAGTCGAGCGCGCTGCTCCACCT--GGAGA 142

Qy 520 CGATGCCGCCCAACGATGTATGGACAGTTGTTGGTACCTTCGATAGTGGCAGCATAGT 579

Db 141 GCGCGGCGCCAGCTGTAGTGCATTGTCACATGTCACAAAGTGGCAGCATGAGT 82
 QY 580 GAAAGTCAAAA 591
 Db 81 AACAGTCAAAA 70

RESULT 13
 US-08-456-265A-4/c
 ; Sequence 4, Application US/08456265A
 ; Patent No. 5767369
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander, Danny C.
 ; APPLICANT: Ryals, John A.
 ; APPLICANT: Goodman, Robert M.
 ; APPLICANT: Stinson, Jeffrey R.
 ; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 ; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 111
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CIBA-GEIGY Corporation
 ; STREET: 520 White Plains Road, P.O. Box 2005
 ; CITY: Tarrytown
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10591

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/456,265A
 ; FILING DATE: 31-MAY-95
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/181,271
 ; FILING DATE: 13-JAN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/093,301
 ; FILING DATE: 16-JUL-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/937,197
 ; FILING DATE: 6-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/678,378
 ; FILING DATE: 1-APR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/305,566
 ; FILING DATE: 6-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/165,667
 ; FILING DATE: 8-MAR-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/042,847
 ; FILING DATE: 6-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/532,441
 ; FILING DATE: 21-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/425,504
 ; FILING DATE: 20-OCT-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/848,506
 ; FILING DATE: 6-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/768,122
 ; FILING DATE: 27-SEP-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/580,431
 ; FILING DATE: 7-SEP-1990
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8587
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 900 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-456-265A-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;
 Best Local Similarity 60.5%; Pred. No. 7.4e-27;
 Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;

QY 46 GGTATCTTTGTTGAAAAAATTTGAAAAAGACGTAGGACACAT-----GGACCTTGGG 99
 Db 607 GGCATCTTTCTTTAAAAAATCTCGCAAATCAGTAGGCCACATGATCCAGGCCCATTTG 548
 QY 100 TGCACAAATATTGTTGCTCTCCAAATGTGGTCAAGGATTGTACATCTCCGGGTACTT 159
 Db 547 TACACATATATTCAITGGTTTTTATCACAGTACATGGGTTGTATCATCCACCTTGTGTTT 488
 QY 160 TAAAGTTGACAGCGGATTCACCATTTATATTTGCGGTGCATTGAATTGTGTGCATTTCC 219
 Db 487 TCACTGTCTGGCATTTGTTCTTAAAGTGTCTGTGTCATCTGAGATTACGACAT---- 432
 QY 220 CTCACCTTGGATTAGTCGGGGGAAAAGTCACTCGGTATATTAAATCCATCAACTAAAGAAA 279
 Db 431 -----CCTCCATTGGTGGGCTGAATTCATGGGATGTTAAATCCATCAACAAGAGA 377
 QY 280 TGTCCCGAAATCTAAGTTGTTGAATGCTTCAAGCGTACTCGGCTAGGGTGTGTTGGTG 339
 Db 376 TGTGCAAAAGTC---CTGATTGGGTTGATTAAAGTCAAAATTCAGCTAAAGTGTAGGTG 320
 QY 340 GTTTGCCCCCAGCGGTGCACTGCAGGACACACCACCAATCACAGTCATGCACGACCTC 399
 Db 319 CTTTTCATAGCTTTGACACTCTAACATCCCGTTACAGTCTCAGTCTCACAAATTACCTC 260
 QY 400 TACCAGCACCATCGAAGTTTACATCCAGTACGACCCCATATATCTGCCATCGTAGTCCCC 459
 Db 259 GGCCACTGCCATCGAAGTTGCAATTTGGTTCGACCCCAAAATCGAGCCTGGAGCTTCCTG 200
 QY 460 TAGGGCATCAATGACCCACATTTGSCCCCGATCGAAAGCTCGGACCCCGCTTCGGGT 519
 Db 199 GGTTCATTAATGCTTCAAGATTGCGCTGAGTCGAGCGCGCTGCTCCACCT--GGAGA 142
 QY 520 CGATCGCGCCCAACGATGATGAGCAGTTGTGGTGTACCTCGATAGTGGCAGCATAGT 579
 Db 141 GGCCGGCGGCCAGACTGTGTAGGTGCATTTGTTGACAAATGTCAAAGTGGCAGCATGAGT 82
 QY 580 GAAAGTCAAAA 591
 Db 81 AACAGTCAAAA 70

RESULT 14
 US-08-455-416-4/c
 ; Sequence 4, Application US/08455416
 ; Patent No. 5777200

GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-455-416-4
Query Match 9.7%; Score 155.2; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 7.4e-27;
Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;
QY 46 GGTATCTTTTGTGAAAAAATGGAAGAAGACGTAGGACACAT-----GGACCTTTGGG 99
Db 607 GGCATCTTTTCTTAAAAAATCTCGACAAATCAGTAGGCCACATGATCCAGGCCCATTTG 548
QY 100 TCGACAATATTTGTCTCTCAAAATGTGTACAGGATTTGTTACATCTCTCCGGTACTT 159
Db 547 TACACAATATTTCTGTTTATTCACAGTACATGGTTGTTTACATCCACCTTTGTTT 488
QY 160 TAAGTTGACAGGGCATTCACATTTATTTATTTGCGGTGATGAATGTTGTTGGCATTTCC 219
Db 487 TCAACTGTCTGGGCATTTGTTTCTTAATAGGTGCTGTGCATCTGAGATTACGACAT---- 432
QY 220 CTCACATTTGATTAGTGGGGCGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAA 279
Db 431 -----CTCCATTTGTCGGGTGATTTCCATGGGGATTTAATCCATCAACAAGAGA 377
QY 280 TGTCACAGAAATCTAAGTTGTTGAACCTGGTCCAGGGGTACTCGGGTAGGGTGTGTTGGTG 339
Db 376 TGTGACAAAGTC---CTGATTGGGTTGATTAAAGTGCAAAATTCAGCTAAAGTTAGGTG 320
QY 340 GTTTGCCCCACCCGGTGCATCTGAGGACACCAACCAATACCATGATGATGACGAACTC 399
Db 319 CTTTTCATAGCTTTGACACTCTAACATCCCGTTACAGTCTCCAGTCTCACAAATACCTC 260
QY 400 TACCAGCACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTGCCTC 459
Db 259 GGCCTATGCCATCGAAGTTGCAATTTGGTTCGACCCCAATCGAGCCCTGGACTGTTCTG 200
QY 460 TAGGGCATCAATGACCCACATTTGGCCCCCATCGAAGCTCGGACCCCGTTCGGGGT 519
Db 199 GGTTCACATTAATGCTCCAAAGATTGGCCTGAGTGGCCGCTGCTCCACCT--GGAGA 142
QY 520 CGATGCCGCCCAACGATGATGGACAGTTGTTGGTACCTTCGATAGTGGCAGCATAGT 579
Db 141 GCGCGGCGCCGACGATGTTAGTGCATTTGTTGACATGTCAAAAGTGGCAGCATGAT 82
QY 580 GAAAGTCAAAA 591
Db 81 AACAGTCAAAA 70

RESULT 15
US-08-455-244-4/c
; Sequence 4, Application US/08455244
; Patent No. 5789214

GENERAL INFORMATION:
APPLICANT: Rvals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr. Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIORITY APPLICATION DATA: US 07/580,431
FILING DATE: 7-SEP-1990
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-455-244-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 7.4e-27;
Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;
QY 46 GGTATCTTTGTTGAAAAAATGGAAAAAGAGCTAGGACCAAT-----GGACCTGGG 99
Db 607 GGCATCTTTTCTTAAAAAATCTGCAAAATCATAGTAGGCCCAATGATCAGGCCCACTTG 548
QY 100 TGCACAAATATTGTTGCTCTCCAAATGTTGGTACAAAGGATTGTACATCTCCGGGTACTT 159
Db 547 TACACAAATATTGTTGTTTATACAGTACATGGGTTGTATACATCCACTTGTGTTT 488
QY 160 TAAGTTGACAGGCGCATTCACCAATTTATATTTGCCGTGCATTGAATTTGTGGCATTTCC 219
Db 487 TCAACTGTCTGGGCATTGTTCTGTTAATAGGTGCTGTGCATCTGAGATTACGACAT---- 432
QY 220 CTCCACTTGGATTAGTCGGGGCGAAGTCATCGGTATATTAATCCATCAACTAAGAAA 279
Db 431 -----CCTCCATTGTCGGGGCTGAATTCATGGGATGTTAAATCCATCAACAAGAGA 377
QY 280 TGTCCAGAAATCTAAGTTGTTGAACTGGTCCAGCGCTACTCGGCTAGGGTGTGTTGGTG 339
Db 376 TGTGACAAAGTC---CTGATTGGGTGATTAAAGTGCAATTCAGCTAAGTGTAGGTG 320
QY 340 GTTTGCCCCACCCGGTGCACTGCAGGACACACCAATCACTACCTCATGACGACACCTC 399
Db 319 CTTTTCATAGCCTTGACACTCTAACATCCCGTTACAGTCTCCAGTCTCACAATTTACCTC 260
QY 400 TACCAGCACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTCCCC 459
Db 259 GGCCTAGTCATCGAAGTTGCAATTTGGTTGACCCCAATTCGAGCCTGAGCTGTTCTGT 200
QY 460 TAGGCGCATCAATGACCCCAATTTGGCCCCGATCGAAACGTCGGCACCCGCTTTCCGGGT 519
Db 199 GGTTCACATTAATGCTGCCAAGATTGGCCTGAGTCAGCGCGCTGCTCCACCT--GGAGA 142
QY 520 CGATCCGCCCAACGATGTATGGACAGTTGTTGGTACCTCGATAGTGGGACGATAGT 579
Db 141 GGCCCGCGCCAGACTGTAGGTGCATTTGTTGCAATGTCAAAAGTGGCAGCATGAT 82
QY 580 GAAAGTCACAAA 591
Db 81 AACAGCTACAAA 70

Search completed: August 18, 2004, 16:17:34
Job time : 126.848 secs

OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 05:06:40 ; Search time 3750.05 Seconds
(without alignments)
12701.209 Million cell updates/sec

Title: US-10-051-307-1

Perfect score: 1595

Sequence: 1 gtaatagactcaactatagg.....tggtgaagtgggtgtttc 1595

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_atc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	488.2	30.6	899	14	CK252883
C 2	488.2	30.6	1004	14	CK248798
C 3	485	30.4	988	14	CK246326
C 4	483.2	30.3	888	14	CK278032

C 5	482.6	30.3	853	14	CK371811
C 6	482.2	30.2	899	14	CK252271
C 7	478.8	30.0	739	12	BI176339
C 8	470.2	29.5	649	9	AW039873
C 9	468.8	29.4	583	12	BI432833
C 10	465.8	29.2	622	10	BF053678
C 11	465.2	29.2	639	12	BI130690
C 12	463.2	29.0	637	12	BI322472
C 13	460.8	28.9	585	9	AW031249
C 14	457.2	28.7	598	14	CA514039
C 15	454.4	28.5	583	9	AW032915
C 16	452.8	28.4	923	14	CK273930
C 17	451.4	28.3	651	10	AW218785
C 18	450.4	28.2	777	12	BM407898
C 19	449.4	28.2	566	9	AW033588
C 20	447.8	28.1	649	10	AW222204
C 21	447.8	28.1	652	12	BI921170
C 22	447.8	28.1	669	12	BI921735
C 23	447.8	28.1	782	12	BM410787
C 24	445.4	27.9	944	14	CK271145
C 25	441	27.6	936	14	CK277819
C 26	439.4	27.5	916	14	CK272733
C 27	438.8	27.5	657	10	AW223507
C 28	437.8	27.4	776	12	BI123660
C 29	437.6	27.4	638	12	BI434454
C 30	437.6	27.3	757	12	BI434095
C 31	435.6	27.3	575	12	BI421330
C 32	434.6	27.2	574	10	AW441774
C 33	434.4	27.2	639	12	BI433955
C 34	434.4	27.2	660	12	BM403979
C 35	433.8	27.2	604	12	BI423179
C 36	433.8	27.2	637	12	BI921311
C 37	433.8	27.2	719	12	BI422260
C 38	433.8	27.2	720	12	BI921826
C 39	433.8	27.2	807	12	BI421946
C 40	433	27.1	574	10	AW223623
C 41	432.8	27.1	626	9	AW033829
C 42	432.2	27.1	629	10	BE432710
C 43	431.8	27.1	682	10	AW223970
C 44	431.8	27.1	710	9	AW035171
C 45	431.6	27.1	573	9	AW032317

ALIGNMENTS

RESULT 1
CK252883/c
LOCUS
DEFINITION
EST736520 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone F0CC086 5' end, mRNA sequence.
ACCESSION
CK252883
VERSION
CK252883.1 GI:39807285
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 899)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
AUTHORS
Generation of ESTs from potato callus tissue
JOURNAL
Unpublished (2003)
COMMENT
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTC ACA CTA TAG.
Location/Qualifiers
1..899
/organism="Solanum tuberosum"
/mol_type="mRNA"


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Db      10 TATATTTT 2

RESULT 3
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LOCUS
DEFINITION
EST729963 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POCAL08 5' end, mRNA sequence.
ACCESSION
CK246326
VERSION
CK246326.1 GI:39793747
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 988)
AUTHORS
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE
Generation of ESTs from potato callus tissue
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: EST729964
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
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Location/Qualifiers
1..988
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCAL08"
/tissue_type="callus"
/lab_host="DH10B-Tona"
/clone_lib="potato callus cDNA library, normalized and
full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."

ORIGIN
Query Match 30.4%; Score 485; DB 14; Length 988;
Best Local Similarity 89.0%; Pred. No. 1.5e-90;
Matches 535; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

QY 46 GGTATCTTTGTTGAAAAAATGGAAAGACGTAGGACCACTGGACCTTGGGTGCAAC 105
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
601 GGCATCTTTGTTGAAAAAATCTAGACAAATCAGTAGGACCACTGGGTGCAAC 542
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
106 AATATTGTTGTCCTCCAAATGTGTACAAAGATTGTTACATCTCCGGGTACTTTAAGTT 165
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
541 AATATTGTTGTCCTCCGAACTGTGTACAGGATTGTTACATCTCCAGGTACCTTAAGTG 482
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
166 GACAGGGCATTCACCATTTATTTGCGGTGCAATTGAATTTGTGGCATTTCCCTCCAC 225
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 AACAGGACATTCACCATTTATTTAGCGGTGCAATGAATTTGCGTGGCATTTCCCTCCAC 422
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
226 TTGGATTAGTCGGGCGGAAGTCATCGGTATTTAAATCCATCACTAAAGAAATGCC 285
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 TAGGATTGTTGGGCGAAAGTCATCGGAATTTAAATCCATCACTAAAGAAATGCC 362
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
286 AGAATCTAAGTTGTGAACCTGGTCCAGGCGTACTCGGTAGGCTTTGGTGGTTTC 345
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 AGAATCTAAGTTGTGAACCTGGTCCAGGCGTATTTCAGCCAGGCTTTGGTGGTTTC 302
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
346 CCCACCGGTGCACTGCAGGACACACCAATCACCAGTATCAGCAACCTTACAG 405
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 CCCACCGGTGCACTGCAGGACACACCAATCACCAGTATCAGCAACCTTACAG 242
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
406 CACCATCAAGTTATCATCCAGTAGCAGCCCCATATACCTGCCATCGTAGTCCCTAGCG 465
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db      241 CACCATCAAAAGTTGCAATTAGTAGACGACCCCATATACGTGCCATCTTAGTGCCCTCGGG 182
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
466 CATCAATGACCCACATTTGGCCCCCGATCGAAACGTCGG--CACCCGCTTTTCGGGGTCGATG 524
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 CATTGATAACCCATGCTGCGCTCGATCGAGACGTCGGCCACCGCTATTCGGGGTCGATG 122
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
525 CGCCCAACAGCATGTATGACACAGTTGTTGCGTACCTCGATAGTGGCAGCATAGTCAAG 584
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 CGCCCAACAGCATGTATGACACAGTTGTTGCGTACCTCGATAGTGGCAGCATAGTCAAG 62
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
585 TCACAAAGCAGACAGGAGGAGAAACAAAAGAGATCTCAAGTAGGCCATGTTTGTGAAA 644
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 TCACAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
645 T 645
Db      1 T 1

RESULT 4
CK278032/c
LOCUS
DEFINITION
EST724110 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAE351 5' end, mRNA sequence.
ACCESSION
CK278032
VERSION
CK278032.1 GI:39835010
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 888)
AUTHORS
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE
Generation of ESTs from abiotic stressed potato tissue
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: EST724111
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
source
Location/Qualifiers
1..888
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAE351"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,

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[illegible]

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Query Match      30.0%; Score 478.8; DB 12; Length 739;
Best Local Similarity 89.3%; Pred. No. 3e-89;
Matches 527; Conservative 0; Mismatches 62; Indels 1; Gaps 1;

QY 46 GGTATCTTTGTTGAAATAATTGAAAGAGAGCTAGGACCACTGACCTGGTGGCAAC 105
Db 590 GGCATCTTTGTTGAAATAATTGAAAGAGAGCTAGGACCACTGACCTGGTGGCAAC 531
QY 106 AATATGTTGCTCTCAATATGTTGACAGGATTGTTACATCTCTCGGCTACTTTAAGTT 165
Db 530 AATATGTTGCTCTCAATATGTTGACAGGATTGTTACATCTCTCGGCTACTTTAAGTT 471
QY 166 GACCAAGGCAATTCACATTTATATTTGCGGTCATGTAATGTTGCAATTCCTCCAC 225
Db 470 AACCAAGGCAATTCACATTTATATTTAGCCGTGCAATGAATTCGCTGACATTTCCCTCCAC 411
QY 226 TTGGATTAGTCGGGCGGAAAGTCATCGGTATATTAATPCCATCAACTAAAGAAATGTCCTC 285
Db 410 TAGGATTGTTGGGCGGAAAGTCATCGGAATATTAATPCCATCAACTAAAGAAATGTCCTC 351
QY 286 AGAATCTAAGTTGTTGAACCTGTCAGAGGCTACTCGGCTAGGCTGTTGGTGGTTGC 345
Db 350 AGAATCTAAGTTGTTGAACCTGTCAGAGGCTACTCGGCTAGGCTGTTGGTGGTTGC 291
QY 346 CCCACCCGGTGCACTGCAAGGACACACCACCAATCACCAAGTCATGCAAGAACCTCTACCA 405
Db 290 CCCACCCGGTGCACTGCAAGGACACACCACCAATCACCAAGTCATGCAAGAACCTCTACCA 231
QY 406 CACATCGAAGTTACATCCAGTACGACCCCATATACCTGCGATCGTAGTCCCTTAGCGG 465
Db 230 CACATCGAAGTTACATCCAGTACGACCCCATATACCTGCGATCGTAGTCCCTTAGCGG 171
QY 466 CATCAATGACCAATTTGGCCCGGATGCAAGACCTGCG- GCACCGCTTTTCGGGTCGATG 524
Db 170 CATGATGACCAATTTGGCCCGGATGCAAGACCTGCG- GCACCGCTTTTCGGGTCGATG 111
QY 525 CCGCCCAACGATGATGACAGTTGTTGCGTACCTGCGATGAGTGGCAGCATAAGTGAAG 584
Db 110 CCGCCCAACGATGATGACAGTTGTTGCGTACCTGCGATGAGTGGCAGCATAAGTGAAG 51
QY 585 TCACAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATG 634
Db 50 TCACAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATG 1

RESULT 8
AW039873/c 649 bp mRNA linear EST 18-MAY-2001
LOCUS
DEFINITION E2282346 tomato mixed elicitor, B71 Lycopersicon esculentum cDNA
ACCESSION AW039873
VERSION AW039873.1 GI:5898627
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 649)
REFERENCE
AUTHORS R. Ascenzi, M., He, X., Lyman, J., Holt, I. E., Liang, P., Upton, J.,
Ronning, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Nierman, W.,
Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and
Giovannoni, J.
Generation of ESTs from tomato leaf tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
source Location/Qualifiers
1..649

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/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
/clone="cLET13J13"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="X11-Blue MRF"
/clone_lib="tomato mixed elicitor, B71"
/vector="pBlueScript SK(-); Site 1: EcoR1; Site 2:
Xho1; cLET- Inoculated with a variety of disease response
elicitors. Plants exposed to 2,6 dichloroisocitonic
acid, BTH, jasmonic acid, ethylene, fenthion, BIX,
okadaic acid, or systemin prior to tissue harvest. EcoRI
site was destroyed during cloning."

```

ORIGIN

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Query Match      29.5%; Score 470.2; DB 9; Length 649;
Best Local Similarity 88.3%; Pred. No. 1.9e-87;
Matches 522; Conservative 0; Mismatches 68; Indels 1; Gaps 1;

QY 49 AATCTTTGTTGAAAAAATTGAAAAAGACGTAGGACCACTGACCTGGGTGCAACAAT 108
Db 591 AATCTTTGTTGAAAAAATTGAAAAAGACGTAGGACCACTGACCTGGGTGCAACAAT 532
QY 109 ATTGTTGCTCTCAATATGTTGACAGGATTGTTACATCTCTCGGCTACTTTAAGTTGAC 168
Db 531 ATTGTTGCTCTCAATATGTTGACAGGATTGTTACATCTCTCGGCTACTTTAAGTTGAC 472
QY 169 CAGGCGATTCACATTTATATTTGCGGTCATGTAATGTTGCGATTTCCCTCCACTTG 228
Db 471 CAGGCGATTCACATTTATATTTAGCCGTACATGATGTTGCAATTTCCCTCCACTTG 412
QY 229 GATTAGTCGGGCGGAAAGTCATCGGTATATTAATPCCATCAACTAAAGAAATGTCCTC 288
Db 411 GATTAGTCGGGCGGAAAGTCATCGGAATATTAATPCCATCAACTAAAGAAATGTCCTC 352
QY 289 AATCTAAGTTGTTGAACCTGTCAGAGGCTACTCGGCTAGGCTGTTGGTGGTTGCC 348
Db 351 AATCTAAGTTGTTGAACCTGTCAGAGGCTACTCGGCTAGGCTGTTGGTGGTTGCC 292
QY 349 ACCCGGTGCACTGCAAGGACACCAACCAATCACCAAGTCATGCAAGAACCTCTACCA 408
Db 291 ACCCGGTGCACTGCAAGGACACCAACCAATCACCAAGTCATGCAAGAACCTCTACCA 232
QY 409 CATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTCCCTTAGCGCAT 468
Db 231 CATCGAAGTTGCAATTCGTACGACCCCATATACCTGCCATCGTAGTCCCTTAGCGCAT 172
QY 469 CAATGACCCCAATTTGGCCCGGATCGAAACCTCG- GCACCGCTTTTCGGGTCGATGCCG 527
Db 171 TGATGACCCCAATTTGGCCCGGATCGAAACCTCG- GCACCGCTTTTCGGGTCGATGCCG 112
QY 528 CCCAAACGATGTTGACAGTGTGCTACCTCGATGTTGGCAGCATAAGTGAAGTCA 587
Db 111 CCCGACGCTGTTATGACAGTGTGTTGGCTACTCTCGAAAGTGGCAGCATAAGTGAAGTCA 52
QY 588 CAAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTG 638
Db 51 CAAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTG 1

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RESULT 9

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BI432833/c 583 bp mRNA linear EST 30-APR-2003
LOCUS
DEFINITION EST535594 P. infestans-challenged potato leaf, compatible reaction
Solanum tuberosum cDNA clone PFCW35 5' sequence, mRNA sequence.
ACCESSION BI432833
VERSION BI432833.1 GI:15257523
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```


Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 583)
Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,
Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, Compatible interaction
Unpublished (2000)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
<http://genome.arizona.edu/orders/>
Seq primer: M13F-R.

Location/Qualifiers
1..583
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PPCW35"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/clone_lib="P. infestans-challenged potato leaf,
compatible reaction"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University, Fry lab; sequencing:
The Institute for Genomic Research; Whole plants were
challenged with 20,000 sporangia/ml of the compatible P.
3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen
in liquid nitrogen immediately upon removal. Kennebec
plants showed first symptoms of infection at 48 hours
after inoculation. NOTE: We cannot exclude the
possibility that this sequence is actually derived from
Phytophthora rather than potato."

Query Match	29.4%	Score 468.8	DB 12	Length 583
Best Local Similarity	89.1%	Pred. No. 3.8e-87		
Matches 517	Conservative 0	Mismatches 62	Indels 1	Gaps 1
Qy	67	TGGAAGAAGCGTAGGACCATGGACCTTCGGTGCAACATATTGTGTCTCCAAATG	126	
Db	581	TCGCAAAATCAGTAGGACCATGGACCTTCGGTGCAACATATTGTGTCTCCGAACG	522	
Qy	127	TGGTACAAGGATTTGATCATCTCCGGGTACTTTAAAGTTGACCAAGGCATTCACCAATTTA	186	
Db	521	TGGTACAAGGATTTGATCATCTCCAGGTACCTTAAGTGAACACAGGACATTCACCAATTTA	462	
Qy	187	TATTTCGGCTGCANTGAATTGTGTGGCAATTTCCCTCCACTTTGGNATTAGTCGGGGCGAAG	246	
Db	461	TATTAGCCGTGCAATGAATTCCGTGACATTTCCCTCCACTAGGATTTGGTTGGGGCGAAG	402	
Qy	247	TCATCGGTATTATTAATCCATCAACTAAAGAAATGTCCCAAGAAATCAAAGTTGTGAAC	306	
Db	401	TCATCGGAATATTAAATCCATCGACTAAAGAAATGTCCCAAGAAATCAGTTGTGAAC	342	
Qy	307	GGTCCAAGCGGTACTCGGCTAGGGTGTGGTGGTTTGCCTCCACCCCGTGCACGTGCAGGA	366	
Db	341	GGTCCAAGCGGTACTCGGCTAGGGTGTGGTGGTTTTCCTCCACCCCGGTACATTCGAAGA	282	
Qy	367	CACGACCACAATTCACCAAGTCATGCACGAACCTCTACGACGACCATCGAAGTTACATCCAG	426	
Db	281	CCCACCACAATTCACCAAGTTGGGATGAACTCTTCGCAAGCACCATCAAAAGTTACAATTAG	222	
Qy	427	TACGACCCCATATATCTGCCATCGPAGTGCCCTTAGGCGCATCAATGACCCACATTTGGC	486	
Db	221	TACGACCCCATATACGTGCCATTTTAGTACCCCTCGGCGCATGTATGACCCCATGTCTGCG	162	

QY	487	CCGATCGAAGCTGCG-ACACCGCTTTCCGGGTTCGATGCGCGCCCAACGATGTATGAC	54
DB	161	CTCGATCGAGCTGCGACCGCGCTATCGGGGTTCGATGCGCGCCCAACGATGTATGAC	102
QY	546	AGTTGTTGCGTACCTCGATAGTGGCAGCATAAGTGAAGTCAAAAAAGCAAGAGGGAGA	605
DB	101	AGTTGTTGCGTACCTCGATAGTGGCAGCATAAGTGAAGTCAAAAAAGCAAGAGGAAGA	42
QY	606	AAACAAAGAAGATCTCAAGTAGCCCATGTTTGTGAAT	645
DB	41	AAACAAAGAAGATCTCAAGTAGCCCATGTTTGTGAAT	2
RESULT 10			
BF053678/c			
LOCUS			
DEFINITION			
EST438908 potato leaves and petioles Solanum tuberosum cDNA clone			
cSTB36B20 5' sequence, mRNA sequence.			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Solanum tuberosum (potato)			
REFERENCE			
AUTHORS			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.			
1 (bases 1 to 622)			
van der Hoeven,R.S., Bezzerides J., Holt,I.E., Liang,F., Cho,J., Utterback,T., Hansen,C.L., Dean,B., Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E., Tanksley,S.D. and Baker,B.			
Generation of ESTs from potato leaves and petioles			
Unpublished (2000)			
CONTACT: Robin Buell			
The Institute for Genomic Research			
9712 Medical Center Dr. Rockville, MD 20850, USA			
Email: potato-array@igr.org			
This clone can be obtained from the University of Arizona Genomics			
Institute. Orders can be made through URL:			
http://genome.arizona.edu/orders/.			
FEATURES			
source			
1..622			
/organism="Solanum tuberosum"			
/mol_type="mRNA"			
/cultivar="Kennebec"			
/db_xref="taxon:4113"			
/clones="cSTB36B20"			
/tissue_type="leaflets and petioles"			
/dev_stages="8 weeks old plants"			
/lab_host="SOLR"			
/clone_lib="potato leaves and petioles"			
/note=vector: pBlueScript SK(-); Site 1: EcoRI; Site 2: XhoI; Tissue was supplied by Dr. Fry (Cornell University)			
Leaflets and petioles were isolated from 8 week old			
greenhouse grown plants. The plants were watered and			
fertilized freely. The tissue was immediately frozen in			
liquid nitrogen."			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
520; Conservative			
29.2%; Score 465.8; DB 10; Length 622;			
87.7%; Pred. No. 1.6e-86;			
Mismatches			
72; Indels			
1; Gaps			
QY	46	GGTATCTTTGTTTGAATAAATCGAGTAGGACCAATGCTTGGGTGCAC	105
DB	602	GGCATCTTTGTTTGAATAAATCTCGACCACTAGTAGGACCAATGCTTGGGTGCAC	543
QY	106	AATATGTTGTCCTCAATATGGTACAGGATCTTACATCCTCGGGTACTTTAAGTT	165
DB	542	AATATGTTGTCCTCTGAACGTGTGACAGGATCTTACATCCTCGGGTACTTTAAGTT	483
QY	156	GACCAAGGCATTCACCATTTTATTTGCGTGCATTAAGTTGTGGGCAATTCCTCCAC	225
DB	482	GACCAAGGCATTCACCATTTTATTTGCGGTGCATTAAGTTGTGGGCAATTCCTCCAC	423

QY 226 TTGGATTAGTCGGGCGGAAGTCATCGGTATATTAATCCATCAACTAAGAAATGTCCTC 285
 Db 422 TAGGATTGGTCGGGCGGAAGTCATCGGTATATTAATCCATCAACTAAGAAATGTCCTC 363
 QY 286 AGAAATCTAAGTTGTTGAAGTGGTCCAAAGGGGTACTCGGCTAGGGTGTGTTGGTGGTTCG 345
 Db 362 AGAAATCTAAGTTGTTGAAGTGGTCCAAAGGGGTACTCGGCTAGGGTGTGTTGGGCGGTTAC 303
 QY 346 CCCACCCGGTCAGTCAGGACACCCACCAATCACCAGTCATCAGCAACCTTACAG 405
 Db 302 CCCACCCGGTCAGTCAGGACCTCACCAATCACCAGTCATCAGCAACCTTACAG 243
 QY 406 CACCATCAAGTTACATCCAGTCAGACCCCATATACCTGCGTAGTGCCTTAGGG 465
 Db 242 CACCATCAAGTTGCAATTAGTACGACCCCATATACCTGCGTAGTGCCTTAGGG 193
 QY 466 CATCATGACCCCATATTTGGCCCGATGCAAACTCGG-CHACCCGCTTTGGGGTTCGATG 524
 Db 182 CATCATGACCCCATATTTGACCTCGATCGAGACGTGCGCCACCCCTTATCGGGTTGATG 123
 QY 525 CCGCCCAACGATGATGGACAGTTGTTGCGTACTCGATAGTGGCAGCATAAAGTGAAG 584
 Db 122 CGCCCGACCGGTGATGGACAGTTGTTGCGACTCAAGAGAGTAGCATATAGTATAAG 63
 QY 585 TCACAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTT 637
 Db 62 TCACAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTT 10

RESULT 11
 BGI30690/c
 LOCUS
 DEFINITION
 EST463582 tomato crown gall Lycopersicon esculentum cDNA clone
 cTOE1A9 5' sequence similar to putative pathogenesis-related
 protein PR P23, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Lycopersicon esculentum (tomato)
 Lycopersicon esculentum
 Eukaryota; Viridiplantae;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 639)

van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Hansen,C.,
 Ronning,C. and Tanksley,S.
 Generation of ESTs from tomato crown gall tissue
 Unpublished (2001)
 Contact: CUGI

TITLE
 JOURNAL
 COMMENT
 Clemson University
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES
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 1..639
 Location/Qualifiers
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cTOE1A9"
 /tissue_type="crown gall"
 /dev_stage="crown galls from full-grown plants (8 wks
 old)"
 /lab_host="SOLR"
 /clone_lib="tomato crown gall"
 /notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; Four wk old greenhouse plants were stab inoculated
 on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr,
 Cornell U.). Galls were allowed to develop for another 4
 wks, when gall tissue was frozen in liquid nitrogen."

ORIGIN

Query Match 29.2%; Score 465.2; DB 12; Length 639;
 Best Local Similarity 88.2%; Pred. No. 2.1e-86;
 Matches 517; Conservative 0; Mismatches 68; Indels 1; Gaps 1;
 QY 49 ATCTTTGTTTGAATAAATTTGGAAGAACGCTAGAGACCATGACCTTTGGGTGCAACAAT 108
 Db 587 ATCTTTGTTTGAATAAATCTCGACAATCAGTAGGGCCACATGGACCTTGTGTGCAACAAT 528
 QY 109 ATGTGTCTCTCAATGTGTGTACAGGATTTGTATCATCTCTCGGGTACTTTAAGTTGAC 168
 Db 527 ATGTGTCTCTCGAACGTTGTGTACAGGATTTGTATCATCTCTCGGGTACCTTAAGTGAAC 468
 QY 169 CAGGGCATTACCATTTATTTGCGGTGCTATTAATTTGTGTGGCATTTCCCTCCACTTG 228
 Db 467 CAGGACATTCACCATTTATTTAGCCGTACATGATTTGCATGGCATTTCCCTCCACTAG 408
 QY 229 GATTAGTCGGGCGGAAGTCATTCGGTATATTAAATCCATCAACTAAAGAAATGCCACA 288
 Db 407 GATTAGTCGGGCGGAAGTCATTTGGAATATTAAATCCATCGACTAAAGAAATGCCACA 348
 QY 289 ATCTAAGTTGTTGAACCTGGTCCAAAGCGTACTCGGCTAGGTTGTTGGTGGTTCGCC 348
 Db 347 ATCTAAGTTGTTGAACCTGGTCCAAAGCGTACTCGGCGAGGTTGTTGGTGGTTCGCC 288
 QY 349 ACCCGGTGCACTGCAAGGACACCCACCAATCACCAGTCATGCAGCAACCTCTACCAGCAC 408
 Db 287 ACCCGGTGCACTTGCAGAGACCCACCAATCACCAGTCATGCAGCAACCTCTACCAGCAC 228
 QY 409 CATCGAAGTTACATTCAGTAGACCCCATATACCTGCCATCGTAGTGGCCCTTAGGGCGAT 468
 Db 227 CATCGAAGTTGCAATTCGTACGCCCATATACCTGCCATCGTAGTGGCCCTTAGGGCGAT 168
 QY 469 CAATGACCCACATTTGGCCCGCATCGAAACGTCG-GCAACCCGCTTTGGGGTTCATGCGG 527
 Db 167 TGATGACCCATGTTTGGCTCGATCAAGCTCGACACCCGCTTATGGGGTTCAGCGCG 108
 QY 528 CCCAAACGATGTATGGACAGTTGTTGCTACTCTCGATAGTGGCAGCATTAAGTGAAGTCA 587
 Db 107 CCCAGACGGTGTATGGACAGTTGTTGCTACTCTCGAAAGTGGCAGCATTAAGTGAAGTCA 48
 QY 588 CAAAAGCAAGAGGAGAGAAACAAAGAGATCTCAAGTAGCCCAT 633
 Db 47 CAAAAGCAAGAGGAGAGAAACAAAGAGATCTCAAGTAGGCCAT 2

RESULT 12
 BGI22472/c
 LOCUS
 DEFINITION
 EST542376 tomato callus Lycopersicon esculentum cDNA clone
 CLSC77J15 5' end, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Lycopersicon esculentum (tomato)
 Lycopersicon esculentum
 Eukaryota; Viridiplantae;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 667)

Alcala,J., Vrebalov,J., White,R., Vision,T., Karameycheva,S.A.,
 Tsai,J., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M.,
 Martin,G.B., Tanksley,S.D. and Giovannoni,J.
 Generation of ESTs from tomato callus tissue (2001)
 Unpublished (2001)
 Contact: CUGI

TITLE
 JOURNAL
 COMMENT
 Clemson University
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 This clone is available through the Clemson University Genomics
 Institute
 Seq primer: T3.
 Location/Qualifiers

FEATURES


```

QY 546 AGTTGTTGGTACCTCGATAGTGGCAGCATAGTCAAGTCAAGTCAAAAAGCAGAGGGAGA 605
Db |||||
QY 103 AGTTGTTGGTACCTCGAAAGTGGCAGCATAGTGTAAAGTCAAAAAGCAGAGGAAGA 44
Db |||||
QY 606 AAACAAAAGAAGATCTCAAGTAGGCCATGTTTGTGTAATTT 647
Db |||||
QY 43 AAACAAAAGAAGATCTCAAGTAGGCCATGTTTGTGGAACAT 2
Db |||||

RESULT 14
CA514039/c
LOCUS 598 bp mRNA linear EST 15-NOV-2002
DEFINITION KS09015D01 KS09 Capsicum annum cDNA, mRNA sequence.
ACCESSION CA514039
VERSION CA514039.1 GI:25014596
KEYWORDS EST.
SOURCE Capsicum annum
ORGANISM Capsicum annum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 598)
AUTHORS Lee, S.-Y., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S.,
Hur, C.-G. and Choi, D.
TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen
JOURNAL Unpublished (2001)
COMMENT Contact: Doil Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doil@mail.kr.ibm.re.kr
Plate: 015 row: D column: 01.

FEATURES
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/mol_type="mRNA"
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/clone_lib="KS09"

ORIGIN
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Best Local Similarity 86.7%; Pred. No. 9.8e-85;
Matches 515; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 46 GGTATCTTTGTTTGA AAAAATTGGA AAGACGTAGGACCAATGGACCTTTGGGTGCAAC 105
Db |||||
QY 594 GGCATCTTTCTTGA AAAAATTGGA AACTCAGTAGGACCAATGGACCTTTGGGTGCAAC 535
Db |||||
QY 106 AATATTGTTGTCCTCA AATGTGTGTA CAGGATTTGTATCTCTCCGGGTACTTTAAGTT 165
Db |||||
QY 534 AATATTGTTGTCCTCA AATGTGTGTA CAGGATTTGTATCTCTCTGGTACCTCGATG 475
Db |||||
QY 166 GACCAGGGCATTCACAT TTTATTTATTTCCCGTGCA TTGAATGTGTCATTTCCCTCCAC 225
Db |||||
QY 474 AACAGGGCATTCACAT TTTATTTATTTCCCGTGCA TTGAATGTGTCATTTCCCAACAC 415
Db |||||
QY 226 TTGATTAGTTCGGGGG GAAAGTCA TCGGTATATTAATCCATCAATTAAGAAATGTCCC 285
Db |||||
QY 414 TAGGATTGTCGGTGC GAAAGTCA TCGGTATATTTGAATCATGACTAAGAAATGTCCC 355
Db |||||
QY 286 AGAAATCTAGTTGTTG AACTGTGTC CAGCGCTACTCGGCTAGGGTGTGTTGGTGTTC 345
Db |||||
QY 354 AGAAATCTAGTTGTTG AACTGTGTT CAGCGCTACTCGGCTAGGGTGTGTTGGTGTTC 295
Db |||||
QY 346 CCCACCCGGTGCAC TG CAGGACAC CACCAATCA CACGAGTCATG CAGCACTCTACCAAG 405
Db |||||
QY 294 CCCACCCGGTGCAC TG CAGGACAC CACCAATCA CACGAGTCATG CAGCACTCTACCAAG 235
Db |||||
QY 406 CACCATCGAAGTTAC ATCCAGTACG ACCCATAT AACTGTCATCTG TGTAGTCCCTTAGGCG 465
Db |||||

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Db 234 AACCATCGAAGTTGCA ATTAGTACACCCCATATAGTGGCCATCGCTGTCCCTGGTGGG 175
QY 466 CATCAATGACCCACAC ATTTGGCCCCGATCGAAACGTGCGCACCCCGTTTC-GGGGTCTGATG 524
Db |||||
QY 174 CATTGATGTCAGGTCTG GCTCTGGCTCGATCAAGAGCTGCGACCGCCACCTACGGGGTCTGATG 115
Db |||||
QY 525 CGCCCCAAACGATGTATG GACAGTTGTTGCGTACCTCGATCTCGATAGTGGCAGCATAGTGAAG 584
Db |||||
QY 114 CGCCCCAAACGATGTATG GACAGTTGTTGCGGACCTCGAAAGTGGCAGCATAGTGAAG 55
Db |||||
QY 585 TCACAAAAGCAGAGGAGG AGGAGAAACAAAAGAGATCTCAAGTAGGCCATGTTTG 638
Db |||||
QY 54 TCACAAAAGCTAGAGAAG AAGAGACAAAAGATGATCTCAATAGGCCATGTTTG 1

RESULT 15
AW032915/c
LOCUS 583 bp mRNA linear EST 18-MAY-2001
DEFINITION EST276474 tomato callus, TAMU Lycopersicon esculentum cDNA clone
ACCESSION CLECI623, mRNA sequence.
VERSION AW032915
KEYWORDS AW032915.1 GI:5891671
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Lycopersicon.
REFERENCE 1 (bases 1 to 583)
AUTHORS Alcala, J., Vrebalov, J., White, R., Matern, A. L., Vision, T.,
Holt, I. E., Liang, F., Upton, J., Craven, M. B., Bowman, C. L., Ahn, S.,
Ronning, C. M., Fraser, C. M., Martin, G. B., Tanksley, S. D. and
Giovannoni, J.
TITLE Generation of ESTs from tomato callus tissue
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.

FEATURES
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/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLECI623"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRF"
/clone_lib="tomato callus, TAMU"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"

ORIGIN
Query Match 28.5%; Score 454.4; DB 9; Length 583;
Best Local Similarity 87.6%; Pred. No. 3.8e-84;
Matches 508; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 67 TCGAAAAGACGTAGGAC CACATGGCTTGGGTGCAACAATATTGTTGCTCTCAATG 126
Db |||||
QY 581 TCGCAAAATCAGTAGGGG CCAATGGACCTTGTGTGCAACAATATTGTTGCTCTCGAAGC 522
Db |||||
QY 127 TGGTACAGGATTTGTTAC ATCTCCGGGTACTTTAAAGTTCAGCCGGCATTCACCATTTA 186
Db |||||
QY 521 TGGTACAGGATTTGTTAC ATCTCCGGGTACTTTAAAGTTCAGCCGGCATTCACCATTTA 462
Db |||||

```

Qy	187	TATTTGCGGTGCATTTGAATTTGTTGGCATTTCCCTCOACTTTGGATTAGTCGGGGCGAAAG	246
Db	461	TATTTAGCCGTACAAATGAATTTGCATTTCCCTCCACTAGGATTTGGTCCGGGGCGAAAG	402
Qy	247	TCATCGGTATATTAAATCCATCAACTAAAGAAATGTCACAGAAATCTAAAGTTGTTGAATCT	306
Db	401	TCATTTGGAATATTAAATCCATTCGATTAAGAAATGTCACAGAAATCTAGTGTTCCTAAATCT	342
Qy	307	GGTCCAAAGCGTACTCGGCTAGGCTGTTTGGTGGTTTGGCCCAACCCGGTGCATTCGAGGA	366
Db	341	GGTCCAAAGCGTACTCGGCGCAGGGTGTGTTGGTGGTTTGGCCCAACCCGGTACATTTGCAAGA	282
Qy	367	CACACCAACAATCACCAAGTCATGCACGAACTCTACAGACCAATCGAAGTTACATCCAG	426
Db	281	CCCCACCAATCACCAAGTCTGACATGAACCTCTACCAGACCACTCAAGTTGCAAAATTCG	222
Qy	427	TACGACCCCATATACCTGCATCTGAGTGCCTTAGCGGCATCAATGACCCCATTTGGC	486
Db	221	TACGACCCCATATACGTGCCATCTTAGTGCCTTCGTGCATTCATGATGACCCATGTTTGGC	162
Qy	487	CCCGATCGAAAAGTGC - GCACCCGCTTTCCGGGTGCGATGCGGCCCAACGATGTATGGAC	545
Db	161	CTCGATCAAGAGCTGCACCAACCGCTATTGTTGGGTTCGACCGCCCGACACGGTGTATGGAC	102
Qy	546	AGTTGTTGGGTACTCTCGATAGTGGCAGCATAAAGTGAAAGTCACAAAAAGCAAGAAAGGAGA	605
Db	101	AGTTGTTGGGTACTCTCGAAGTTGGCAGCATTAAGTGTAACTCAGAAAGCAAGAAAGGAGA	42
Qy	606	AAACAAAAAGATCTCAAGTAGGCCATGTTGTTGGAAAT	645
Db	41	AAACACACAGAAGATCTCAAGTAGGCCATGTTGTTGGAACT	2

Search completed: August 18, 2004, 16:04:23
Job time : 3756.05 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 03:35:10 ; Search time 6053.11 Seconds
(without alignments)
11442.406 Million cell updates/sec

Title: US-10-051-307-2
Perfect score: 1598
Sequence: 1 gtaatagactcactatagg.....tggtgaagtgggtgctttc 1598

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ats.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_on.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_ats.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1598	100.0	1598	6	AX665979 Sequence
2	1482.2	92.8	1595	6	AX665978 Sequence
3	1334.4	83.5	1546	6	AX665980 Sequence
C 4	689.6	43.2	2659	8	SC81OLP
C 5	531.4	33.3	2638	8	SC13OLP
C 6	525.8	32.9	1304	8	AF093743
C 7	477.4	29.9	901	8	AF093743 Lycopersi
C 8	469.2	29.4	2033	8	SC05MLP
C 9	468.8	29.3	1549	8	NTAP24G
C 10	468.8	29.3	3033	6	AR037158 Sequence
C 11	468.8	29.3	3033	8	S40046
C 12	449.8	28.1	729	8	AF473702 Solanum n
C 13	449.6	28.1	917	8	AY093595 Lycopersi
C 14	449.4	28.1	744	8	AF450276 Solanum n
C 15	448.4	28.1	818	8	AY007309 Solanum d
C 16	446.6	27.9	977	8	SCA81OLP
C 17	440.2	27.5	937	8	AF297646 Capsicum
C 18	438	27.4	856	8	CAN297410
C 19	425.6	26.6	832	8	LEPM1M
C 20	419.8	26.3	883	6	AL6780
C 21	419.8	26.3	883	6	AR027097 Sequence
C 22	419.8	26.3	883	6	AR103205 Sequence
C 23	419.8	26.3	884	6	AL6782
C 24	419.8	26.3	884	6	AR027098 Sequence
C 25	419.8	26.3	884	6	AR103206 Sequence
C 26	419.8	26.3	961	8	NTAP24
C 27	419	26.2	845	8	LEPRPA
C 28	417.8	26.1	741	6	A83550
C 29	417.8	26.1	741	6	BD082734
C 30	414	25.9	928	8	S44889
C 31	412.6	25.8	917	8	TOMNP24
C 32	398.8	25.0	971	8	AF376058
C 33	391.8	24.5	738	8	NTOSMOTIN
C 34	388.6	24.3	541	8	AY256440
C 35	388.4	24.3	542	8	AY256441
C 36	387.8	24.3	593	8	AY256429
C 37	387.4	24.2	567	8	AY256439
C 38	386.6	24.2	526	8	AY256436
C 39	386.2	24.2	538	8	AY256431
C 40	383.8	24.0	535	8	AY256434
C 41	382	23.9	510	8	AY256425
C 42	382	23.9	539	8	AY256430
C 43	380.8	23.8	621	8	AF450277
C 44	378.4	23.7	561	8	AF548357
C 45	375.4	23.5	3127	8	TOBNP50

ALIGNMENTS

RESULT 1
AX665979
LOCUS AX665979 1598 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2 from Patent WO02059333.
ACCESSION AX665979
VERSION AX665979.1 GI:29290848
KEYWORDS
SOURCE Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1
AUTHORS Dai,Z., Shi,L. and Hooker,B.S.
TITLE Gene promoters isolated from potato and use thereof

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 02059333-A 2 01-AUG-2002;
Dai, Ziyu (US); Shi, Lifang (US); Hooker, Brian, S. (US)

FEATURES
Location/Qualifiers

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/organism="Solanum tuberosum"
/mol_type="unassigned DNA"
/db_xref="taxon:4113"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATATACGACTCAGTATAGGACGCGCTGGTGCAGCGCGCGGCTGGTATCTTTGTTGA 60
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QY 61 AAAAATTGGAAGAAAGAGTAGGACACATGGACCTTGGGTGCAACAATATGTTCCTC 120
DB 61 AAAAATTGGAAGAAAGAGTAGGACACATGGACCTTGGGTGCAACAATATGTTCCTC 120

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QY 181 CATTATATTTCCGCTGCANTGAATGTTGGCAATTTCCCTCCACTTGGATAGTCGGGG 240
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QY 241 CGAAGTCATCGGTATATTAATCCATCACTAAGAAATGTCGCCAAGATCTAAGTTGT 300
DB 241 CGAAGTCATCGGTATATTAATCCATCACTAAGAAATGTCGCCAAGATCTAAGTTGT 300

QY 301 TGAATGCTGCTCAAGCGCTACTCGGCTAGGCTGTTTGGTGGTTTGGCCGCCACCCGGTGCAC 360
DB 301 TGAATGCTGCTCAAGCGCTACTCGGCTAGGCTGTTTGGTGGTTTGGCCGCCACCCGGTGCAC 360

QY 361 GCAGACACACCAATCACTAGCTGATGACGAACTCTACGACGACGACGACGACGAC 420
DB 361 GCAGACACACCAATCACTAGCTGATGACGAACTCTACGACGACGACGACGACGAC 420

QY 421 ATCCAGTACGACCCCATATATCGTCCATCGTATGTCGCTTGGCCGCCACCCGGTGCAC 480
DB 421 ATCCAGTACGACCCCATATATCGTCCATCGTATGTCGCTTGGCCGCCACCCGGTGCAC 480

QY 481 TTTGGCTCGATCGAGAGCTCGGCGACCGGCTATCGGGTGCATGCGGCGCATCGATGTA 540
DB 481 TTTGGCTCGATCGAGAGCTCGGCGACCGGCTATCGGGTGCATGCGGCGCATCGATGTA 540

QY 541 TGGACAGTTGTTGGCGGTACCTCGATAGTGCAGCATAAGTGAAGTCAACAAGCCAGA 600
DB 541 TGGACAGTTGTTGGCGGTACCTCGATAGTGCAGCATAAGTGAAGTCAACAAGCCAGA 600

QY 601 AGGAGAAACCAAGAAAGATCTCAAGTACGACGACGACGACGACGACGACGACGAC 660
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QY 661 AATTATTTTGGTACTTATATAGGATATGCGGCTTTGGCCTACGACGATATTAAT 720
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DB 841 ATATAGCCTATAGTTACAGTTAACTTTATTTGGTGATTAACCTTTGACATATAAATCTGT 900

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DB 901 AACGTGACGGAATTTTCTTAAACTAAATATTTAAAGACGACTATTTTCACTTTTTCG 960

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DB 961 TGGCCAAAGTCTCTGTCATCTATCTATGCGCAATTTTACTTTTATCGTTCTAGCCTTC 1020

QY 1021 TAGGTACACAGTTTGAACATAAAATAATCAATAAAATTTGAAAGTAAATAATTTAGTTT 1080
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DB 1141 TTTAAATTCACAAACCATTTCTGCTAATGGGGAAGTCTATGATTCGTGGCAAGTGTTC 1200

QY 1201 ATTATTTCTAGTCTAGATTCGAGTCAACATTTTGTAGTCAAAATATCTATTTAAAGAACCC 1260
DB 1201 ATTATTTCTAGTCTAGATTCGAGTCAACATTTTGTAGTCAAAATATCTATTTAAAGAACCC 1260

QY 1261 CTATTTGATGCAAAATATCTATTTAAAGAACCCCTATTCATCTTTTATTTTACGATC 1320
DB 1261 CTATTTGATGCAAAATATCTATTTAAAGAACCCCTATTCATCTTTTATTTTACGATC 1320

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DB 1321 GGAGCATGGATATATTTACTAATTTAAATAAAATTTGGGAGGAATTCATCGAACCAAGTC 1380

QY 1381 AGCTTATGCTGATCCACATTTAGGATACGTTAGTATGCTGTTTATAGAAACCAAGTC 1440
DB 1381 AGCTTATGCTGATCCACATTTAGGATACGTTAGTATGCTGTTTATAGAAACCAAGTC 1440

QY 1441 GATCATGTACAAATGAGTTTAAATAATCTCTCTATAAATACCTGTCTATCCCTCTTAAAC 1500
DB 1441 GATCATGTACAAATGAGTTTAAATAATCTCTCTATAAATACCTGTCTATCCCTCTTAAAC 1500

QY 1501 CAAATACATCTTAAACACAAATAATTAACCTTAGATTCCTTAAAGAAATTCAGAAATTA 1560
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QY 1561 TGGAGGCAAAATAAGTCTATGTTGAAAGTTGGTTGCTTTC 1598
DB 1561 TGGAGGCAAAATAAGTCTATGTTGAAAGTTGGTTGCTTTC 1598

RESULT 2

AX665978 1595 bp DNA linear PAT 26-MAR-2003
Sequence 1 from Patent WO02059333.

AX665978

AX665978.1 GI:29290847

KEYWORDS

SOURCE

ORGANISM

Solanum tuberosum (potato)

Solanum tuberosum

Spemacophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Solanum.

1

Dai, Z., Shi, L. and Hooker, B.S.

Gene promoters isolated from potato and use thereof

Patent: WO 02059333-A 1 01-AUG-2002;

Dai, Ziyu (US); Shi, Lifang (US); Hooker, Brian, S. (US)

Location/Qualifiers

1..1598

/organism="Solanum tuberosum"

/mol_type="unassigned DNA"

/db_xref="taxon:4113"

FEATURES

source

ORIGIN


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Query Match      92.8%; Score 1482.2; DB 6; Length 1595;
Best Local Similarity 96.7%; Pred No. 2.5e-298;
Matches 1546; Conservative 0; Mismatches 48; Indels 5; Gaps 3;

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DB 1 GTAATACGACTCAGTATAGGACACGCGTGGTCGACGCGCGTGGTATCTTTGTTGA 60

QY 61 AAAAATTCGAAAGAACCTAGGACACATGACACCTGGTGGTCAACAATTTGTTGCTC 120
DB 61 AAAAATTCGAAAGAACCTAGGACACATGACACCTGGTGGTCAACAATTTGTTGCTC 120

QY 121 CAAATGTCGTACAGGATTTTACATCCTCCGGGTACTTTAAAGTGAAGTACAGCAATTCAC 180
DB 121 CAAATGTCGTACAGGATTTTACATCCTCCGGGTACTTTAAAGTGAAGTACAGCAATTCAC 180

QY 181 CATTTATATTTGCCGTGCAATTTGAATTTGTTGGCATTTCCCTCCACTTGGATTTAGTCGGG 240
DB 181 CATTTATATTTGCCGTGCAATTTGAATTTGTTGGCATTTCCCTCCACTTGGATTTAGTCGGG 240

QY 241 CGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCACAGAAATCTAAGTTGT 300
DB 241 CGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCACAGAAATCTAAGTTGT 300

QY 301 TGAATCGTCCAGGCGTACTCGGCTAGGCTGTTGGTGGTTTGGCCCAACCCGGTGCAT 360
DB 301 TGAATCGTCCAGGCGTACTCGGCTAGGCTGTTGGTGGTTTGGCCCAACCCGGTGCAT 360

QY 361 CGAGACACACCAATCAGCTATGACGACGACCTTACAGCAGCCAGCAGGATAC 420
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QY 421 ATCCAGTACGACCCCATATAGTGCATCGTAGTGCCTTAGGCGCATCAATGACCCACA 480
DB 421 ATCCAGTACGACCCCATATAGTGCATCGTAGTGCCTTAGGCGCATCAATGACCCACA 480

QY 481 TTTGGCCCTCGATCGAGACGTCGGGACCGCTATCGGTCGATCGCGCCCAACGATGTA 540
DB 481 TTTGGCCCGATCGAAACGTCGGGACCGCTTTCGGGTCGATCGCGCCCAACGATGTA 540

QY 541 TGGACAGTTGTTGGCGTACCTCGATAGTACAGCATAGTAAAGTCAAAAAGCCAGA 600
DB 541 TGGACAGTTGTTG - CGTACCTCGATAGTGCAGCATAGTAAAGTCAAAAAGCCAGA 598

QY 601 AGGAGAAACCAAAGAGATCTCAAGTAGCCCATGTTGTTGAAATTTATATGTGACA 660
DB 599 AGGAGAAACCAAAGAGATCTCAAGTAGCCCATGTTGTTGAAATTTATATGTGACA 658

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QY 721 CGTATTTATACAAATATCATCTTTGACTAATTATAAACGAAATATATTACATATGAT 780
DB 719 CGTATTTATAGCAATATCATCTTTGACTAATTATAAACGAAATATATTACATATGAT 778

QY 781 TTGTTAACGTTGAGTGGAAATATGATATAGAGCGGCTTAATTAATTTATTTATGA 840
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QY 841 ATATAGCCTATAGTTTACAAGTTAACTTTATTTGTTGATACCTTTGACATATAACTCTGT 900
DB 839 ATATAGCCTATAGTTTACAAGTTAACTTTATTTGTTGATACCTTTGACATATAACTCTGT 898

QY 901 AACGTGACGGAATTTTCTTAAATCTAATATTAATAAGAGCAGCTATTTTACATTTTCG 960
DB 899 AACGTGACGGAATTTTCTTAAATCTAATATTAATAAGAGCAGCTATTTTACATTTTCG 958

QY 961 TGGCCAAAGTCTTTGCACTATCTATGCGCATTTTCTTTTATCTTTTATCTGTTAGCCCTC 1020
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QY 1021 TAGGTACAGTTTGAACATAAAAAATCATAAAAATTTGAAAGTAAAAATTTAGTTTTTTT 1080
DB 1019 TAGGTACAGTTTGAACATAAAAAATCATAAAAATTTGAAAGTAAAAATTTAGTTTTTTT 1078

QY 1081 TTCAATTTACTCGTATGGATCAATTTGTTAGATCAATCTGAAATATACAAACCAATTCGAT 1140
DB 1079 TTCAATTTACTCGTATGGATCAATTTGTTAGATCAATCTGAAATATACAAACCAATTCGAT 1138

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DB 1139 TTTAAATACACACCAATTCCTTAATTTGGGAGTCTATGTTGTTGTTGTTGTTGTTGTTGTT 1196

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QY 1380 AGCTTTATCGTCGATCCACATTTAGGATAACGTTAGTATGGCTGTTTATAGAGAAACAAGT 1439
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QY 1440 GGATCATGTACATTTGAGTTTAAATATCTCTTATAAATACCTGCTCTCTCTTAA 1499
DB 1437 GGATCATGTATATTTAGTTTAAATATCTCTTATAAATACCTGCTCTCTCTTAA 1496

QY 1500 CCAATATCATCTAACACACAAATATAAATTTAGATTTCTTAAAGAAATTTGAGAAATTA 1559
DB 1497 CTAATATCATCTAACACACAAATATAAATTTAGATTTCTTAAAGAAATTTGAGAAATTA 1556

QY 1560 ATGAGGCAATTAAGTCTATGTTGAGGTTGGTCTTTTC 1598
DB 1557 ATGAGGCAATTAAGTCTATGTTGAGGTTGGTCTTTTC 1595

RESULT 3
LOCUS AX665980 1546 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 3 from Patent WO02059333.
ACCESSION AX665980
VERSION AX665980.1 GI:29290849
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum
REFERENCE 1
AUTHORS Dai, Z., Shi, L. and Hooker, B.S.
TITLE Gene promoters isolated from potato and use thereof
JOURNAL Patent: WO 02059333-A 3 01-AUG-2002;
FEATURES Dai, Ziyu (US); Shi, Lifang (US); Hooker, Brian, S. (US)
source Location/Qualifiers
1. .1546
/organism="Solanum tuberosum"
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ORIGIN

Query Match 83.5%; Score 1334.4; DB 6; Length 1546;
Best Local Similarity 93.8%; Pred. No. 1.5e-267;
Matches 1456; Conservative 0; Mismatches 87; Indels 10; Gaps 6;

QY 49 ATCTTTGTTGAAAAATTTGAAAGACACCTAGGACCATGACCTTGGTGCACAAAT 108
DB 1 ATCTTTGTTGAAAAATTTGAAAGACACCTAGGACCATGACCTTGGTGCACAAAT 60

QY 109 ATTGTTGCTCTCCAAATGTGTACAGGATTTGTATATCTCCCGGTACTTTAAGCTGAC 168
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1246 CTATTAAAGAACCCCTATTGATCAATATCTATTAAAGAACCCCTATTCTACTACTTTTA 1305
1196 CTATTAAAGAACCCCTATTGATGCAAAAGTCAATAAA--TATTAAATATCATNCITTA 1253
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1366 ATCGACAGCCATCAAGCTTATCGTCGATCCACATAGGATAAAGTTAGTAGTGGCTGTTT 1425
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1486 CTATCCCTCTTAAACAAATACATCAACACAAATATATAAATAGTATCTCTTAAGA 1545
1434 ATATACCTCTAAACCTAAATGATCACTAAACACAAATATATAAATAGTATCTCTTAAGA 1493
1546 AATTGCAGAAATTAATGAGGCAAAATAGTCTATGTTGAAGTTGGTTGCTTTC 1598
1494 AATTGCAGAAATTAATGAGGCAAAATAGTCTATGTTGAAGTTGGTTGCTTTC 1546

RESULT 4
SC810LP/c 2659 bp DNA linear PLN 27-OCT-1995
DEFINITION S.commersonii (posML81) gene for osmotin-like protein.
LOCUS X72927.1 GI:296773
VERSION osmotin-like protein.
KEYWORDS Solanum commersonii (Commerson's wild potato)
SOURCE Solanum commersonii
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1
Zhu, B., Chen, T.H. and Li, P.H.
AUTHORS Activation of two osmotin-like protein genes by abiotic stimuli and
TITLE fungal pathogen in transgenic potato plants
JOURNAL Plant Physiol. 108 (3), 929-937 (1995)
MEDLINE 95357444
PUBMED 7630973
REFERENCE 2 (bases 1 to 2659)
AUTHORS Zhu, B.
TITLE Direct Submission
JOURNAL Submitted (29-MAR-1993) B. Zhu, Oregon State University, Dept of
Horticulture, AG & Life Science 4017, Corvallis, OR 97331, USA
COMMENT Related sequences: M29279 & M21346.
FEATURES
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TATA_signal
mRNA
CDS

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361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCTTAGGGGCAT 420
469 CAATGACCCCATTTGGCGTCGATCGAGAGCGTGGGGCAGCGCTATC-GGGTCGATGCCG 527
421 CAATGACCCCATTTGGCGTCGATCGAGAGCGTGGGGCAGCGCTATC-GGGGTGCGATGCTG 480
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828 AATTATTTTATGAATATAGCTATAGTTTACAAAGTTAACTTTATTTGGTGATACTTTGAC 887
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948 TTCAATTTTTCGGGGCAAGTCTCTTGATATCTTATCTATGCCCCATTTTACTTTTAT 1007
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1008 CGTTCTAGCCTTCTAGGTACGTTTGAACATATAAATAATATAAATTTGAAGTGAATAA 1067
959 CGTTCTAGCCTTCTAGGTACGTTTGAACATATAAATAATATAAATTTGAAGTGAATAA 1018
1068 TTAGTTTTTTTTTTCATATTAATCTCGATGATCATTTGTTAGATCAATCTGAATATATC 1127
1019 TTAG--TTTTTTTTTTCATATTAATCTCGATGATCATTTGTTAGATCAATCTGAATATATC 1075
1128 AAACCATTTCTGATTTTAAATTCACCAACCATTTCTGCCCTAATGGGGAAGTCTAT-GTATTC 1186
1076 AAATCATTTCTGATTTTAAATTCATACTATTTCTCATGATGGGAACGCTCATGGTATTC 1135
1187 GTGCAAGTGTGTA-TTATTTCTAGTCTAGATTTGGAGTCACAACTTTTACTGCAAAATAT 1245

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ORIGIN

Query Match 43.2%; Score 689.6; DB 8; Length 2659;
 Best Local Similarity 73.5%; Pred. No. 2.7e-133; Indels 217; Gaps 13;
 Matches 1156; Conservative 0; Mismatches 199;

QY 46 GGTATCTTTGTTGAAAAATTTGAAAAAGACGTAGGACCAACATCGGACCTTGGGTGCAAC 105
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QY 106 AATATTTGTTCTTCCCAATGTGTACAAGATTTGTATCATCTCCCGGTACTTTAAGCT 165
 DB 1615 AATATTTGTTCTTCCCAATGTGTACAAGATTTGTATCATCTCCCGGTACTTTAAGGG 1556

QY 166 GACTAGGACATTCACATTTATTTGCGGTGCAATTTGAATTTGTGGCATTTCCCTCCAC 225
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QY 226 TTGGATTTAGTCGGGCGAAAGTCATCGGTATTTAAATCCATCACTAAAGAAATGTCCT 285
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QY 525 CGGCCAAACGATGATGCAAGTTGTTGGCGGTACCTCGATGATGACAGCATTAAGTGAA 584
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QY 585 AGTCACAAAGCCAGAGGGAGAACCAAAAGAGTCTCAAGTAGCCCATGTT---TG 640
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QY 934 ---AAAAAGCAGTATTTTCACTTTTTCGTGGCCAAAGTCTTGTGCATCTTATCTATG 990
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QY 1051 AAAATTGAAAGTAATAAATTAGTTTATTTTTCATATTACTC---CTATGGATCATTTGT 1107
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QY 1527 AACTTAGATTCTTTAAAGAAATTTGAGAATTTAAATGGAGGCAAAATAGTCTATGTTGAAG 1586
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RESULT 5
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 DEFINITION X72928
 ACCESSION X72928.1 GI:296771
 VERSION cmotin-like protein.
 KEYWORDS Solanum commersonii (Commerson's wild potato)
 SOURCE Solanum commersonii
 ORGANISM Solanum commersonii

REFERENCE 1
 Zhu, B., Chen, T. H. and Li, P. H.
 Activation of two osmotin-like protein genes by abiotic stimuli and
 fungal pathogen in transgenic potato plants
 JOURNAL Plant Physiol. 108 (3), 929-937 (1995)
 MEDLINE 95357444
 PUBMED 7630973

REFERENCE 2 (bases 1 to 2638)
 Zhu, B.
 Direct Submission
 Submitted (29-MAR-1993) B. Zhu, Oregon State University, Dept of
 Horticulture, AG. & Life Science 4017, Corvallis, OR 97331, USA
 Related sequences: M29279 & M21346.
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Best Local Similarity 76.1%; Pred. No. 2.4e-100; Indels 28; Gaps 5;
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RESULT 6
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LOCUS
DEFINITION
Lycopersicon esculentum pathogenesis-related protein osmotin
precursor (NP24) gene, complete cds.
ACCESSION
AF093743
VERSION
AF093743.1 GI:3747059
KEYWORDS
SOURCE
ORGANISM
Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE
1 (bases 1 to 1304)
Jia,Y. and Martin,G.B.
Rapid transcript accumulation of pathogenesis-related genes during
an incompatible interaction in bacterial speck disease-resistant
tomato plants
Plant Mol. Biol. 40 (3), 455-465 (1999)
JOURNAL
MEDLINE
PUBMED
10437829
REFERENCE
2 (bases 1 to 1304)
Martin,G.B. and Jia,Y.
Direct Submission
JOURNAL
SUBMITTED (22-SEP-1998) Boyce Thompson Institute, Tower Road,
Ithaca, NY 14853-1801, USA
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QY 946 TTTTTCAC 952
Db 24 TCGTGAC 18
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RESULT 7
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LOCUS S.commersonii mRNA for osmotin-like protein.
DEFINITION X67121
ACCESSION X67121
VERSION X67121.1 GI:21194
KEYWORDS osmotin-like protein.
SOURCE Solanum commersonii (Commerson's wild potato)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
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REFERENCE 1 (bases 1 to 901)
AUTHORS Zhu,B., Chen,T.H. and Li,P.H.
TITLE Expression of an ABA-responsive osmotin-like gene during the
induction of freezing tolerance in Solanum commersonii
JOURNAL Plant Mol. Biol. 21 (4), 729-735 (1993)
MEDLINE 93192535
PUBMED 8448373
REFERENCE 2 (bases 1 to 901)
AUTHORS Zhu,B.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1992) B. Zhu, Dept of Horticulture, AG & Life
Science 4017, Oregon State University, Corvallis OR 97331, USA
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1 (bases 1 to 901)
Zhu,B., Chen,T.H. and Li,P.H.
Expression of an ABA-responsive osmotin-like gene during the
induction of freezing tolerance in Solanum commersonii
JOURNAL Plant Mol. Biol. 21 (4), 729-735 (1993)
MEDLINE 93192535
PUBMED 8448373
2 (bases 1 to 901)
Zhu,B.
Direct Submission
Submitted (02-JUL-1992) B. Zhu, Dept of Horticulture, AG & Life
Science 4017, Oregon State University, Corvallis OR 97331, USA
Location/Qualifiers
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Db      11  A 11

RESULT 8
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LOCUS   NTOSPR N.tabacum osmotin gene. 2033 bp DNA linear PLN 01-FEB-1996
DEFINITION
ACCESSION X95308
VERSION X95308.1 GI:1167853
KEYWORDS osmotin; PR protein.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE
1 Barnard, W.M. and Neale, A.D.
Comparison of the 5 regulatory regions of homeologous osmotin genes
from Nicotiana tabacum
Neale, A.D.
Direct Submission
Submitted (24-JAN-1996) A.D. Neale, Monash University, Genetics and
Developmental Biology, Wellington Rd, Clayton, Victoria, 3168,
Australia

FEATURES
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QY      106  AATATCTTGTCTCCAAATGTGGTCAAGAGTTGTTACATCTCCGGGTPACITTAAGCT 165
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Db      1325  CATTGATCACCCCAAGTTTGGCTCGATCGAGGCGTCGGGCCACCCGCTATGGGGGTGCAAG 1266
QY      525  CCGGCCAAACGATGTATCGACAGTTGTTGGCGGTACCTCGATAGTGCAGCATAAAGTAA 584
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QY      645  AATTTATATGTGGACAAATTTTGTGTAATTTATATATAGGATAGCGGCGCTTTT-- 702
Db      1147  CATTTCTTTTAAACAGTTGCGTTTGGGATATAGTGACAAATTTTGTGGTTTATAT 1088
QY      703  -----GGCACTACGGATATTAATCGTATTATATATAACAATATCATATCTTACTA 751
Db      1087  AGGAGTAGTGGCGGCTTTTCGCACATAGACATTAATCATATATATATTTATTAACTTGA 1028
QY      752  ATTATAACGAAATATATTACAATATGATTTGGTAAAGCTTGAGTGGGAAATATATAA 811
Db      1027  CTAGTAAATGGATATTTCTCAAGGATGCTTTAGTAAAGGTGAGCGCGCTAAAAAGTATA 968
QY      812  GAGCGCGCTAAT--AATTAATTTATTTATGAATATAGCCTATAGTTACAAAGTTAACTTAT 870
Db      967  GAGCGCGCTAATTAACATTAATTTTATGATATAG-----AAGTCAATTTAT 920
QY      871  TTGGTGATAACTTTGACATATAAACTCTGTAAACGTGAC 908
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RESULT 9
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LOCUS   N.tabacum ap24 gene.
DEFINITION
ACCESSION X65701
VERSION X65701.1 GI:19782
KEYWORDS osmotin.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE
1 Melchers, L.S., Sela-Buurlage, M.B., Vloemans, S.A., Woloshuk, C.P.,
Van Roekel, J.S., Pep, J., van den Elzen, P.J. and Cornelissen, B.J.
Extracellular targeting of the vacuolar tobacco proteins AP24,
chitinase and beta-1,3-glucanase in transgenic plants
Plant Mol. Biol. 21 (4), 583-593 (1993)
93192519

```

PUBMED 8448358
 REFERENCE 2 (bases 1 to 1549)
 AUTHORS Melchers, L.S.
 TITLE Direct Submission
 JOURNAL Submitted (24-APR-1992) L.S. Melchers, Mogen International NV, Einsteinweg 97, 2333 CB Leiden, THE NETHERLANDS
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 1027 GGCATCTTTGTTGAAAATTTGAAAAGACGTAGGACACATGACCTTGGGTGCAAC 968
 106 AATATTTGTTGCTCCCAATGTGTACAAAGATGTTTACATCTCCCGGTACTTTAAGCT 165
 967 AATATTTGTTGCTCCCAATGTGTACAAAGATGTTTACATCTCCCGGTACTTTAAGCT 908
 166 GACTAGGACATTCACCATTTATTTGCGTGCATTTGAATTTGTTGGCATTTCCCTCCAC 225
 907 CGCGGGGACATTCGCGCGTTTATTTAGCCGTACCAATGAATTTGATTTCCCTCCAC 848
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 257 AACATAAGACCGCCTAATAATAATTTATTTTATGTAATATAG-----AAGTCA 210
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 DEFINITION Sequence 1 from patent US 5801028.
 ACCESSION AR037158
 VERSION AR037158.1 GI:5955014
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES
 1 (bases 1 to 3033)
 Bressan, R. and Hasegawa, P.M.
 TITLE Camotrin gene promoter and use thereof
 JOURNAL Patent: US 5801028-A 1 01-SEP-1998;
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 Best Local Similarity 76.8%; Pred. No. 2.6e-87;
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Qy 865 CTTTATTTGGTGATAACTTTGACATATAAACTCTGTACAGTGAC 908
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RESULT 12
AF473702/c
LOCUS AF473702 729 bp DNA linear PLN 25-FEB-2002
DEFINITION Solanum nigrum osmotin-like protein gene, complete cds.
ACCESSION AF473702
VERSION AF473702.1 GI:19874518
KEYWORDS
SOURCE
ORGANISM Solanum nigrum (black nightshade)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
AUTHORS Jami,S.K. and Kirti,P.B.
TITLE PCR-based cloning of an osmotin-like protein gene from Solanum
nigrum
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 729)
AUTHORS Jami,S.K. and Kirti,P.B.
DIRECT SUBMISSION
JOURNAL Direct Submission
SUBMITTED (21-JAN-2002) Department of Plant Sciences, University of
Hyderabad, Gachibowli, Hyderabad, A.P 500046, India
FEATURES
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Matches 516; Conservative 0; Mismatches 72; Indels 3; Gaps 2;

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Db 529 AATATTGTTGCTCCGACGTTGGTACAGGATGTTTACATCTCCGGTACTCTAAGTG 470
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RESULT 13
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LOCUS AY093595 917 bp mRNA linear PLN 17-OCT-2002
DEFINITION Lycopersicon esculentum PR-5x (PR-5) mRNA, complete cds.
ACCESSION AY093595
VERSION AY093595.1 GI:20750096
KEYWORDS
SOURCE
ORGANISM Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 917)
Rep,M., Dekker,H.L., Vossen,J.H., De Boer,A.D., Houterman,P.M.,
Speijter,D., Back,J.W., De Koster,C.G. and Cornelissen,B.J.C.
Mass Spectrometric Identification of Isoforms of PR Proteins in
Xylem Sap of Fungus-Infected Tomato
Plant Physiol. 130 (2), 904-917 (2002)
22264016
12376655
2 (bases 1 to 917)
Rep,M., Dekker,H., Vossen,J.H., de Boer,A., Houterman,P.,
Speijter,D., Back,J.-W. and Cornelissen,B.J.C.
Direct Submission
Submitted (28-NAR-2002) Plant Pathology, University of Amsterdam,
Kruislaan 318, Amsterdam 1098SM, Netherlands
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DB 70 AGTCACAAAAGCCAGAGGAGAAATAAAAGAGATGTCAAGTAGGCCCATGTTTGTGA 11
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DB 10 CATATTTTG 1

RESULT 14
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LOCUS
DEFINITION Solanum nigrum osmotin-like protein precursor (OIP) gene, complete cds.
ACCESSION AF450276
VERSION AF450276.1 GI:19401630
KEYWORDS
SOURCE Solanum nigrum (black nightshade)
ORGANISM Solanum nigrum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 744)
Campos,M.A., Ribeiro,S.G., Rigden,D.J., Monte,D.C. and Grossi de
Sa,M.F.
TITLE Pathogenesis related-like genes of Solanum nigrum: cloning and
characterization of genes coding for neutral and basic PR5-like
proteins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 744)
AUTHORS Campos,M.A., Ribeiro,S.G., Monte,D.C. and Grossi de Sa,M.F.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2001) PBI, Embrapa Genetic Resources and
Biotechnology, P.O. Box 02372, Brasilia, DF 70770-900, Brazil
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DB 589 GGCATCTTTGTTGAAAATTTTGCAATTCGAGGACCACTGGGCTTGGGTGCAAC 530
QY 106 AATATTGTTGCTCCCAATTTGTTGACAAAGATTGTTCATCCTCCGGGTACTTTAAGCT 165
DB 529 AATATTGTTGCTCCGAAACGTTGTACAAAGATTGTTCATCCTCCGGGTACTTTAAGTG 470
QY 166 GACTAGGACATTCACCATTTATTTGCGGTGCAATGAATTTGTGTGCAATTCCTCCAC 225
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DB 289 CCCACCGGTGCTAGGACGACACCAACATCACCAGTCATGCATGAACCTCTACCAG 230
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RESULT 15
AY007309/c 818 bp mRNA linear PLN 22-JAN-2001
LOCUS Solanum dulcamara cryoprotective osmotin-like protein mRNA,
DEFINITION complete cds.
ACCESSION AY007309
VERSION AY007309.1 GI:10445202
KEYWORDS
SOURCE Solanum dulcamara
ORGANISM Solanum dulcamara
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 818)
AUTHORS Newton,S.S. and Duman,J.G.
TITLE An osmotin-like cryoprotective protein from the bittersweet
nightshade Solanum dulcamara
JOURNAL Plant Mol. Biol. 44 (5), 581-589 (2000)
MEDLINE 21039368
PUBMED 11198420
REFERENCE 2 (bases 1 to 818)
AUTHORS Newton,S.S. and Duman,J.G.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Biological Sciences, University of Notre
Dame, Galvin Life Sciences Bldg., Notre Dame, IN 46556, USA

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| | | | |
QY 106 AATATGTTGCTCCCAATGTGGTACAAAGATGTTACATCTCCGGGTACTTTAAGCT 165
| | | | |
Db 550 AATATGTTGCTCCCAACGTGGTACAAAGGTGTTACATCTCCGGGCACTCTAAGTG 491
| | | | |
QY 166 GACTAGGACATCCACATTATATTGCGGTGATGAAATGTTGTGGCATTTCCCTCCAC 225
| | | | |
Db 490 AACCAGGACATTCACCATTTATGTTAGCCGTGCAATGAATGCAATGGCAATTTCTCTCCAC 431
| | | | |
QY 226 TTGGATTAGTCGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGCCCC 285
| | | | |
Db 430 TAGGATTGTCGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGCCCC 371
| | | | |
QY 286 AGAAATCTAAGTTGTGAACCTGGTCCAGGCGTACTCGGCTAGGTTGCTGGTTGCG 345
| | | | |

Db 370 AGAAATCTAGGTTGCTGAACTGGTCCAGGCATATTCGGCCAGGGGTGTTTGGGGGTTTGC 311
| | | | |
QY 346 CCCACCCGGTGCACCTGCAGGACACACACATCACCAGTCAATGCACGAACCTCTACCCAG 405
| | | | |
Db 310 CCCACCCAGTACACTGTAGTACCCACACCAATCACCACTCTGCACACGAACCTCTACCCAG 251
| | | | |
QY 406 CACCAACCGAAGTTTACATCCAGTACGACCCCATATAGTCCCATCGTAGTSCCCCTAGGCG 465
| | | | |
Db 250 CACCATTTGAAGTTTACAACACAGTACGACCCCATATAGTCCCATCTTAGTGCCCTTGGTG 191
| | | | |
QY 466 CATCAATGACCCACATTTGGCCCTCGATCGAGAGGTGGGACCGGCTATC-GGGTCGATG 524
| | | | |
Db 190 CATTGATGACCCCATGTTTGGCCCTCGATCTAGACGTGACCCACCATATCGGGGGTCGACG 131
| | | | |
QY 525 CCGCCCAACAGATGTATGACACAGTGTTCGGCGGTACTCGATAGTACAGCATAAAGTAA 584
| | | | |
Db 130 CCGCCCAACAGTGTACGACAGTGT--TCGGACCTCGATAGTGGCAGCATAAAGTATA 73
| | | | |
QY 585 AGTCACAAAAGCCAGAGGAGGAGAAACCAAAAGAGATCTCAAG---TAGCCCATGTTTGT 641
| | | | |
Db 72 AGTCACAAAAGCAAGGAGGAGGAGAAACCAAAAGATCTCAAGTAATAGCCCATGTTTGT 13
| | | | |
QY 642 TGAATTTTATAT 653
| | | | |
Db 12 GGAACTATTTT 1
| | | | |

Search completed: August 18, 2004, 12:58:35
Job time : 6059.11 secs

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 03:32:09 ; Search time 571.22 Seconds
(without alignments)
11884.422 Million cell updates/sec

Title: US-10-051-307-2

Perfect score: 1598
Sequence: 1 gtaatacagctactactagg.....ttggtgaagtgtgtgttc 1598

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1596.4	99.9	1598	6	Abk90561 Potato pr
2	1480.6	92.7	1595	6	Abk90560 Potato pr
3	1344	84.1	1546	6	Abk90562 Potato pr
C 4	468.8	29.3	3033	2	Aav52754 Nicotiana
C 5	468.8	29.3	3033	2	Aax16340 Tobacco o
C 6	419.8	26.3	883	2	Aaql5269 Osmotin-1
C 7	419.8	26.3	884	2	Aaql5270 Encodes C
C 8	417.8	26.1	741	2	Aav68641 Nucleotid
C 9	355	22.2	1004	2	Aac21414 Encodes o
C 10	189	11.8	906	3	Aac47993 Arabidops
C 11	187.4	11.7	902	3	Aac47227 Arabidops
C 12	186.8	11.7	735	6	Abz14313 Arabidops
C 13	186.8	11.7	735	7	Abz42096 Arabidops
C 14	186.8	11.7	735	7	Ada68525 Arabidops
C 15	186.8	11.7	950	6	Abn98566 Arabidops
C 16	168.8	10.6	875	5	Aac84839 Sunflower
C 17	157	9.8	771	3	Aaz29511 Asparagus
C 18	144.8	9.1	900	1	Aan90842 Fragment
C 19	144.8	9.1	900	2	Aav62808 Tobacco P
C 20	144.8	9.1	900	2	Aav72992 PR-R majo
C 21	138.6	8.7	910	4	Aad04241 Sunflower
C 22	133.2	8.3	549	3	Aac55150 Arabidops
C 23	126.4	7.9	2000	7	Ada71704 Rice gene

ALIGNMENTS

RESULT 1

ABK90561	ABK90561 standard; DNA; 1598 BP.
ID	ABK90561 standard; DNA; 1598 BP.
XX	XX
AC	ABK90561;
XX	XX
DT	15-NOV-2002 (first entry)
XX	XX
DE	Potato proteinase inhibitor 1 (pin1) gene promoter isoform II.
XX	XX
KW	Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
KW	Controlled Environmental Agriculture; crop cultivation.
XX	XX
OS	Solanum tuberosum.
XX	XX
FN	WO200259333-A2.
PD	01-AUG-2002.
XX	XX
PF	18-JAN-2002; 2002WO-US001287.
XX	XX
PR	23-JAN-2001; 2001US-0263224P.
XX	XX
PA	(DAIZ/) DAI Z.
PA	(SHIL/) SHI L.
PA	(HOOK/) HOOKER B S.
XX	XX
PI	Dai Z, Shi L, Hooker BS;
XX	XX
DR	WPI; 2002-608457/65.
XX	XX
PT	New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter
PT	isoforms derived from potato, useful in manipulating expression of genes
PT	and in Controlled Environmental Agriculture for heterologous protein
XX	XX
PS	production.
XX	XX
CC	Claim 2; Fig 2; 43pp; English.
CC	CC
CC	The invention relates to polynucleotides having proteinase inhibitor 1
CC	(pin1) or aminotransferase (amt) gene promoter activity. Isoforms of pin1
CC	and amt gene promoters are useful in manipulating expression of genes,
CC	particularly in transformed plant cells. The gene promoters are useful in
CC	constructing gene expression vectors and in Controlled Environmental
CC	Agriculture for heterologous protein production. The vectors are useful
CC	in facilitating the expression and/or secretion of heterologous proteins
CC	in cell culture or by crop cultivation. The new gene promoter isoforms

Aaq58992 Diospyros
Aaa40422 Potato in
Aaq58991 Diospyros
Aaq6184 PR-R majo
Aaq91491 Zeamatin
Aav28688 Ripening
Aan40215 Gene enco
Ada71063 Rice gene
Ada71064 Rice gene
Abq85936 Arabidops
Abq78707 Nucleotid
Aad59196 Modified
Aan70934 DNA seque
Ada69630 Rice gene
Aaq4913 PING152CV
Aaq4914 PING323CV
Aan70933 DNA seque
Abq78703 Nucleotid
Aad59192 Thaumatin
Aan50328 Sequence
Aat06312 Thaumatin
Aat06311 Thaumatin

C 24 117.8 7.4 627 2 Aaq58992
C 25 116.8 7.3 500 3 Aaa40422
C 26 114.6 7.2 693 2 Aaq58991
C 27 114 7.1 950 2 Aaq6184
C 28 109 6.8 834 2 Aaq91491
C 29 105.6 6.6 808 2 Aav28688
C 30 100.6 6.3 705 1 Aan40215
C 31 99.8 6.2 1970 7 Ada71063
C 32 96.2 6.0 1932 7 Ada71064
C 33 94.2 5.9 343 6 Abq85936
C 34 92.2 5.8 621 6 Abq78707
C 35 92.2 5.8 621 9 Aad59196
C 36 90.8 5.7 669 1 Aan70934
C 37 90.8 5.7 669 7 Ada69630
C 38 90.8 5.7 1309 2 Aaq4913
C 39 90.8 5.7 1309 2 Aaq4914
C 40 89.2 5.6 621 1 Aan70933
C 41 89.2 5.6 621 6 Abq78703
C 42 89.2 5.6 621 9 Aad59192
C 43 89.2 5.6 639 1 Aan50328
C 44 79.8 5.0 624 2 Aat06312
C 45 73.6 4.6 624 2 Aat06311

CC provide high level, stable and controllable expression that is
 CC temporarily, environmentally, or developmentally regulatable. This
 CC sequence represents a potato pin1 gene promoter isoform

SQ Sequence 1598 BP; 507 A; 299 C; 300 G; 492 T; 0 U; 0 Other;

Query Match 99.9%; Score 1596.4; DB 6; Length 1598;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1597; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTATATACGACCTCACTATAGGCGACGCTGGTGCACGCGCCGGGCTGTATCTTTGTTGA 60
 DB 1 GTATATACGACCTCACTATAGGCGACGCTGGTGCACGCGCCGGGCTGTATCTTTGTTGA 60
 QY 61 AAAAATTGGAAGAAAGCGTAGGACCAATGAGACCTTGGGTGCAACAATAATGTTGTCCTC 120
 DB 61 AAAAATTGGAAGAAAGCGTAGGACCAATGAGACCTTGGGTGCAACAATAATGTTGTCCTC 120
 QY 121 CAATATGTTGTTGAGGATGTTATCATCTCCGGGTACTTTAAGCTGACTAGGACATTCAC 180
 DB 121 CAATATGTTGTTGAGGATGTTATCATCTCCGGGTACTTTAAGCTGACTAGGACATTCAC 180
 QY 181 CATTTATATTTGCGGTGCATTTGAATTTGTTGGCATTTTCCCTCCCATTTGGATTAGTCGGG 240
 DB 181 CATTTATATTTGCGGTGCATTTGAATTTGTTGGCATTTTCCCTCCCATTTGGATTAGTCGGG 240
 QY 241 CGAAAGTCATCGGTATATTAATCCATCACTAAAGAAATGTCGCAAGATCTAAGTTGT 300
 DB 241 CGAAAGTCATCGGTATATTAATCCATCACTAAAGAAATGTCGCAAGATCTAAGTTGT 300
 QY 301 TGAATCTGTCACAGCGCTACTCGGCTAGGCTGTTTGGTGTGTTGCGCCACCCCGGTGCAC 360
 DB 301 TGAATCTGTCACAGCGCTACTCGGCTAGGCTGTTTGGTGTGTTGCGCCACCCCGGTGCAC 360
 QY 361 GCAGGACACGACCAATTCAGCTAGTATGACGAGAACCTCTACAGGACACACCGAAGTTAC 420
 DB 361 GCAGGACACGACCAATTCAGCTAGTATGACGAGAACCTCTACAGGACACACCGAAGTTAC 420
 QY 421 ATCCAGTACGACCCCAATATAGTCCCATCTGAGTCCCTTAGGCGCATCAATGACCCACA 480
 DB 421 ATCCAGTACGACCCCAATATAGTCCCATCTGAGTCCCTTAGGCGCATCAATGACCCACA 480
 QY 481 TTTGGCTTCGATCGAGACGTCGGGACCGGCTATCGGGTCGATCGGCGCCCAACGATGTA 540
 DB 481 TTTGGCTTCGATCGAGACGTCGGGACCGGCTATCGGGTCGATCGGCGCCCAACGATGTA 540
 QY 541 TGGACAGTTGTTGGCGGTACTCGATAGTGCACGACATAAGTGAAGTCACAAAGCCGGA 600
 DB 541 TGGACAGTTGTTGGCGGTACTCGATAGTGCACGACATAAGTGAAGTCACAAAGCCGGA 600
 QY 601 AGGAGAGAAACCAAGAGAGTCTCAAGTAGCCCATGTTTGTGAATTTATATGTTGACA 660
 DB 601 AGGAGAGAAACCAAGAGAGTCTCAAGTAGCCCATGTTTGTGAATTTATATGTTGACA 660
 QY 661 AATTAATTTTGGTACTTTATATAGGATATGCGGCTTTTGGCAGTACGGATATTAAT 720
 DB 661 AATTAATTTTGGTACTTTATATAGGATATGCGGCTTTTGGCAGTACGGATATTAAT 720
 QY 721 CGTATTATATAACAATATCATCTTTGACATAATTAAGGAAATATATACAAATATGAT 780
 DB 721 CGTATTATATAACAATATCATCTTTGACATAATTAAGGAAATATATACAAATATGAT 780
 QY 781 TTGTTAAAGCTTGAAGTGGAAAAATGATTAAGAGCCGCTTAATAATTAATTTATGTA 840
 DB 781 TTGTTAAAGCTTGAAGTGGAAAAATGATTAAGAGCCGCTTAATAATTAATTTATGTA 840
 QY 841 ATATAGCTATAGTTTACAAGTTAACTTTATTTGGTGATTAACCTTTGACATATAAATCTGT 900
 DB 841 ATATAGCTATAGTTTACAAGTTAACTTTATTTGGTGATTAACCTTTGACATATAAATCTGT 900
 QY 901 AACGTGACGGAATTTTCTTAAACTAAATATTAATAAGAGCAGTATTTTACATTTTTCG 960
 DB 901 AACGTGACGGAATTTTCTTAAACTAAATATTAATAAGAGCAGTATTTTACATTTTTCG 960

QY 961 TGGCCAAAGTCTCTTTGCACTATCTATATGCCCATTCTTTTATCGTTCTTACGCTTC 1020
 DB 961 TGGCCAAAGTCTCTTTGCACTATCTATATGCCCATTCTTTTATCGTTCTTACGCTTC 1020
 QY 1021 TAGGTACACGTTTGAACATAAAATCATAAATTTGAAGTAAATTTAGTTTCTTTT 1080
 DB 1021 TAGGTACACGTTTGAACATAAAATCATAAATTTGAAGTAAATTTAGTTTCTTTT 1080
 QY 1081 TTCAATATCTCGTATGATCATTTTGTAGTCAATCTGAAATATACAAACCATCTGAT 1140
 DB 1081 TTCAATATCTCGTATGATCATTTTGTAGTCAATCTGAAATATACAAACCATCTGAT 1140
 QY 1141 TTTAAATATCAACCAATCTGCTTAATGGGGAAGTCTATGATTCGTTGGCAAGTTTG 1200
 DB 1141 TTTAAATATCAACCAATCTGCTTAATGGGGAAGTCTATGATTCGTTGGCAAGTTTG 1200
 QY 1201 ATTATTTCTAGTCTAGATTGGAGTCACAACTTTTAGTGCAATATCTATTAAGAAACCC 1260
 DB 1201 ATTATTTCTAGTCTAGATTGGAGTCACAACTTTTAGTGCAATATCTATTAAGAAACCC 1260
 QY 1261 CTATTTGATGCAAAATATCTATTTAAAGAACCCCTATTCATCTTTATTTTACGATC 1320
 DB 1261 CTATTTGATGCAAAATATCTATTTAAAGAACCCCTATTCATCTTTATTTTACGATC 1320
 QY 1321 GGAGCATGATATATTTTACTAATTAATAAATTTGGGAGGAATTTGATCGCAAGCCATCA 1380
 DB 1321 GGAGCATGATATATTTTACTAATTTAAATAAATTTGGGAGGAATTTGATCGCAAGCCATCA 1380
 QY 1381 AGCTTTATCGTGCATCCCAATTAGGATAACGTTAGTAGTGGCTGTTTTAGAGAAACAAAGTG 1440
 DB 1381 AGCTTTATCGTGCATCCCAATTAGGATAACGTTAGTAGTGGCTGTTTTAGAGAAACAAAGTG 1440
 QY 1441 GATCATGTCAATTTGAGTTAAATAATCTCTATTAATATCTCTATCTATCTCTCTTAAAC 1500
 DB 1441 GATCATGTCAATTTGAGTTAAATAATCTCTATTAATATCTCTATCTATCTCTTAAAC 1500
 QY 1501 CAATATACATCTAAACACACAAATATAAATTTAGATTCTTTAAAGAAATTTGAGAAATTTAA 1560
 DB 1501 CAATATACATCTAAACACACAAATATAAATTTAGATTCTTTAAAGAAATTTGAGAAATTTAA 1560
 QY 1561 TGGAGGCAAAATAGTCTATGTTGAGTTGGTTGCTTTC 1598
 DB 1561 TGGAGGCAAAATAGTCTATGTTGAGTTGGTTGCTTTC 1598

RESULT 2
 ABK90560
 ID ABK90560 standard; DNA; 1595 BP.
 XX
 AC ABK90560;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Potato proteinase inhibitor 1 (pin1) gene promoter isoform I.
 XX
 KW Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
 KW Controlled Environmental Agriculture; crop cultivation.
 XX
 OS Solanum tuberosum.
 XX
 PN WO200259333-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 18-JAN-2002; 2002WO-US001287.
 XX
 PR 23-JAN-2001; 2001US-0263224P.
 XX
 PA (DAIZ/) DAI Z.
 PA (SHIL/) SHI L.
 PA (HOOK/) HOOKER B S.
 XX

Dai Z,	Shi L,	Hooker BS;
WPI; 2002-608457/65.		
New proteinase inhibitor 1 (pinl) or aminotransferase (amt) gene promoter isoforms derived from potato, useful in manipulating expression of genes		
and in Controlled Environmental Agriculture for heterologous protein production.		
Claim 2; Fig 1; 49pp; English.		
The invention relates to polynucleotides having proteinase inhibitor 1 (pinl) or aminotransferase (amt) gene promoter activity. Isoforms of pinl (pinl) or amt promoters are useful in manipulating expression of genes, particularly in transformed plant cells. The gene promoters are useful in constructing gene expression vectors and in Controlled Environmental Agriculture for heterologous protein production. The vectors are useful in facilitating the expression and/or secretion of heterologous proteins in cell culture or by crop cultivation. The new gene promoter isoforms provide high level, stable and controllable expression that is temporally, environmentally, or developmentally regulatable. This sequence represents a potato pinl gene promoter isoform		
Sequence 1595 BP; 510 A; 291 C; 297 G; 497 T; 0 U; 0 Other;		
Query Match Best Local Similarity 96.6%; Pred. No. 0; Matches 1545; Conservative 0; Mismatches 49; Indels 5; Gaps 3;		
Qy 1 GTAATAGACTCTATAAGGACCGGTGGTCGAAGCCGCCGTGGTATTCTTTTGTA 60		
Db 1 GTAATAGACTCTATAAGGACCGGTGGTCGAAGCCGCCGTGGTATTCTTTTGTA 60		
Qy 61 AAAAATGAAAAAGAAGTAGAACCAATGCACCCTGGGTGAAACAATATGTTGCTC 120		
Db 61 AAAAATGAAAAAGAAGTAGAACCAATGCACCCTGGGTGAAACAATATGTTGCTC 120		
Qy 121 CAATGTGGTACAAAGATTGTTACATCTCCCGGGTACTTTAAGCTGACTAGGACATTCAC 180		
Db 121 CAATGTGGTACAAAGATTGTTACATCTCCCGGGTACTTTAAGTTGACCGGCAATTCAC 180		
Qy 181 CATTTATATTCCGFGCATGAAATGTTGTGGCATTTCCCTCCACTTGGANTAGTCGGG 240		
Db 181 CATTTATATTCCGFGCATGAAATGTTGTGGCATTTCCCTCCACTTGGANTAGTCGGG 240		
Qy 241 CGAAAGTCATCGGTATATTAATCCATCAAATTAAGAAAATGCCCAGAAAATCTAAGTTGT 300		
Db 241 CGAAAGTCATCGGTATATTAATCCATCAAATTAAGAAAATGCCCAGAAAATCTAAGTTGT 300		
Qy 301 TGAACTGGTCCAAGCGTACTCGGCTAGGCTGTTTTGGTGGTTGCCCCCACCGGTGCACT 360		
Db 301 TGAACTGGTCCAAGCGTACTCGGCTAGGCTGTTTTGGTGGTTGCCCCCACCGGTGCACT 360		
Qy 361 GCAGGACACACCAATACACAGTCATGCAGAACCTCTACAGCACACCGAAGTTAC 420		
Db 361 GCAGGACACCAATACACAGTCATGCAGAACCTCTACAGCACACCGAAGTTAC 420		
Qy 421 ATCCAGTAGCAACCCCATATAGTGGCATGTTAGTGCCTTAGGCGCATCAATAGCCACA 480		
Db 421 ATCCAGTAGCAACCCCATATAGTGGCATGTTAGTGCCTTAGGCGCATCAATAGCCACA 480		
Qy 481 TTITGGCTCGATCGAGACGTCGGGCACCGCTATCGGTGCTGTCGCCCAACAGATGA 540		
Db 481 TTITGGCTCGATCGAANCTGGGCACCGCTTTCCGGGTGCTGTCGCCCAACAGATGA 540		
Qy 541 TGACAGATTGTTGGCGGTACTCTCGATAGTAGCAGCATAAAGTGAAGTCACAAAAGCCAGA 600		
Db 541 TGACAGATTGTTG - -CGTACCTCGATAGTGGCAGCATAAAGTGAAGTCACAAAAGCCAGA 598		
Qy 601 AGGGAGAAACCAAAGACATCTCAAGTAGCCCATGTTGTTGAAATTTATATGTGACA 660		
Db 599 AGGGAGAAACCAAAGACATCTCAAGTAGCCCATGTTGTTGAAATTTATATGTGACA 658		

Potato proteinase inhibitor 1 (pin1) gene promoter isoform III.

Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
Controlled Environmental Agriculture; crop cultivation.

Solanum tuberosum.

WO200259333-A2.

01-AUG-2002.

18-JAN-2002; 2002WO-US001287.

23-JAN-2001; 2001US-0263224P.

(DAIZ/) DAI Z.

(SHIL/) SHI L.

(HOOK) HOOKER B S.

Dai Z, Shi L, Hooker BS;

WPI; 2002-608457/65.

New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter isoforms derived from potato, useful in manipulating expression of genes and in Controlled Environmental Agriculture for heterologous protein production.

Claim 2; Fig 3; 43pp; English.

The invention relates to polynucleotides having proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter activity. Isoforms of pin1 and amt gene promoters are useful in manipulating expression of genes, particularly in transformed plant cells. The gene promoters are useful in constructing gene expression vectors and in Controlled Environmental Agriculture for heterologous protein production. The vectors are useful in facilitating the expression and/or secretion of heterologous proteins in cell culture or by crop cultivation. The new gene promoter isoforms provide high level, stable and controllable expression that is temporarily, environmentally, or developmentally regulatable. This sequence represents a potato pin1 gene promoter isoform

Sequence 1546 BP; 501 A; 270 C; 284 G; 490 T; 0 U; 1 Other;

Query Match 84.1%; Score 1344; DB 6; Length 1546;

Best Local Similarity 94.1%; Pred. No. 5.7e-291;

Matches 1462; Conservative 0; Mismatches 81; Indels 10; Gaps 6;

49 ATCTTTGTTGAAAAAATTGAAAAGAACGTTAGGACACACATGGACCTTGGTGCAACAAT 108

1 ATCTTTGTTGAAAAAATTGAAAAGAACGTTAGGACACACATGGACCTTGGTGCAACAAT 60

109 ATTGTTGCTCCTCAAAATGTGTACAAAGATTGTACATCTCCGGGTACTTTAAGCTGAC 168

61 ATTGTTGCTCCTCAAAATGTGTACAAAGATTGTACATCTCCGGGTACTTTAAGCTGAC 120

169 TAGGACATTACCACTTATATTTCCCGTGCAATTTGTTGGCAATTTCCCTCCCACTTG 228

121 TAGGACATTACCACTTATATTTCCCGTGCAATTTGTTGGCAATTTCCCTCCCACTTG 180

229 GATTAGTGGGGGGAAGTCACTCGGTATATTAATCCATCACTAAAGAATGTCCGAGA 288

181 GATTAGTGGGGGGAAGTCACTCGGTATATTAATCCATCACTAAAGAATGTCCGAGA 240

289 AATCTAAGTTGTTGAACTGTTGCTCAAGCGTACTCGGTAGGTTGTTGGTGGTTTGGCCC 348

241 AATCTAAGTTGTTGAACTGTTGCTCAAGCGTACTCGGTAGGTTGTTGGTGGTTTGGCCC 300

349 ACCCGGTGCACTGAGGACACCAACCAATCAACAGTCATGCAAGAACCTCTACACGAC 408

301 ACCCGGTGCACTGAGGACACCAACCAATCAACAGTCATGCAAGAACCTCTACACGAC 360

409 CACCGAAGTTACATCCAGTACGACCCCATATACGTGCTAGTCCCTTAGGCGCAT 468

361 CATCGAAGTTATCATCCAGTAGCAGCCCATATACGTGCGCATCGTAGTCCCTTAGGCGCAT 420
469 CAATGACCCACATTTGGCTCGATCGAGACGTCGGGACCCGCTATC-GGGTCGATGCGG 527
421 CAATGACCCACGTTTGGCTCGATCGAGACGTCGGGACCCGCTATCGGGTCCATGCTG 480
528 CCCAAACGATGTATGGACAGTTGTTGGCGGTACCTCGATAGTGACAGCATAGTGAAGT 587
481 CCCAGACGCTGTATGGACAGTTGTTG--CGTACCTCGATAGTGGCAGCATAGTGAAGT 538
588 CACAAAGCCAGAGGGGAGAACCAAGAGAGATCTCAAGTAGGCCCATGTTGTTGAAAT 647
539 CACAAAGCCAGAGGGGAGAACCAAGAGAGATCTCAAGTAGGCCCATGTTGTTGAAAT 598
648 TTATATGTGGACAAATATATTTTGGTACTTTATATATAGGGATAGCGGCTTTGGCAC 707
599 TTATATGTGGACAAATATATTTTGGTACTTTATATAGGGATAGCGGCTTTGGCAC 658
708 TACGGATATTAATCGTATATATTAACAATATCATACTTTGACTAATTAATAACGAATAT 767
659 TATGGATATTAATCGTATATTAACAATATCATACTTTGACTAATTAATAACGAATAT 718
768 ATTCAATATGATTTGGTAAACGTTGAGTGGAAAAATGTATAAGAGCCGCTTAATAT 827
719 ATTCAATATGATTTGGTAAACGTTGAGTGGAAAAATGTATAAGAGCCGCTTAATAT 778
828 AATATTTTATGAAATATAGACTATAGTATCAAGTTAACTTTATTTGGTGATACCTTGAC 887
779 AATATTTTATGAAATATAGACTATAGTATCAAGTTAACTTTATTTGGTGATACCTTGAC 838
888 ATATAAACCTGTAAACGTTGAGTGGAAAAATGTATAAGAGCCGCTTAATAT 947
839 ATATAAACCTGTATCGTACGAGGAACTTTCTTAAACTAAATTAATAAGAGCAGCTAT 898
948 TTCAATTTTCTGTTGCGGCAAGTCTCTTGCAATATCTATAGCCCATTTTACTTTTAT 1007
899 TTATATTTTCTGTTGCGGCAAGTCTCTTGCAATATCTATAGCCCATTTTACTTTTAT 958
1008 GCTTCTGCTCTAGGTACAGTTGTAACATAAAATCATAAATTAATAAGAGTGAATAA 1067
959 GCTTCTGCTCTAGGTACAGTTGTAACATAAAATCATAAATTAATAAGAGTGAATAA 1018
1068 TTAGTTTCTTCTATCTACTCGTATGATCATTTGTTAGATCAATCTGAAATATAC 1127
1019 TTAG--TTTCTTCTATCTACTCGTATGATCATTTGTTAGATCAATCTGAAATATAC 1075
1128 AAACCATTTCTGATTTAAATCACAACCATTTCTGCTTAATGGGAGTCTAT-GTGATTC 1186
1076 AAATCATTTCTGATTTAAATCATAACTATTTCTGATGATGGGAACTCTATGTTGATTC 1135
1187 GTGGCAAGTGTGTA-TTATTTCTAGTCTAGATGGAGTCAAACTTTTGTAGTCAAAATAT 1245
1136 GTGACAGTGTGTTGATTTATTTCTAGTCTGATGGAGTCAAACTTTTGTAGTCAAAATAT 1195
1246 CTATTAAGAAACCCCTATTTGATGCAATATCTATTAAGAAACCCCTATTTCACTTTA 1305
1196 CTATTAAGAAACCCCTATTTGATGCAAAAGTCAATAAA--TATTTAATATCAATCTTTA 1253
1306 TTTATTTTACGATCGGAGCATGGATATTTTACTTAATAAAATAAATGGGAGGAAATG 1365
1254 TTTATTTTACGATCGGAGCATGGATATTTTACTTAATAAAATAAATGGGAGGAAATG 1313
1366 ATCGAAGGACCATCAAGCTTATCGTCCGATCCCATTTAGGATAAGCTTAGTATGCTGTT 1425
1314 ATCGAAGGACCATCAAGCTTATCGTCCGATCCCATTTAGGATAAGCTTAGTATGCTGTT 1373
1426 TTAGGAAACAGTGGATCATGTAATTTGAGTTAAATAATATCTCTATAAATACCTGT 1485
1374 TTAGGAAACAGTGGATCATGTAATTTGAGTTTAAATAATATCTCTATAAATATCTAT 1433
1486 CTATCCCTCTTAAACCAAAATACATCTAACACACAAAATATAAATTTAGATTCCTTAAGA 1545

Db 1434 ATATACCTCTAAACCTAAATGCATCTAAACACAAATATAAATTAAGTCTTTAAAGA 1493
 QY 1546 AATTCAGAAATTAATGGAGGCAAAATAAGTCTATCGTGAAGTTGTTCTTTC 1598
 Db 1494 AATTCAGAAATTAATGGAGGCAAAATAAGTCTATCGTGAAGTTGTTCTTTC 1546

RESULT 4
 AAV52754/c
 ID AAV52754 standard; DNA; 3033 BP.

XX AC AAV52754;

XX DT 02-NOV-1998 (first entry)

XX DE Nicotiana tabacum osmotin gene with promoter.

XX KW Nicotiana tabacum; tobacco plant; osmotin gene; promoter; inhibition;
 KW fungal pathogen; insect pathogen; nematode pathogen; viral pathogen; ds.
 XX OS Nicotiana tabacum.

XX FH Key Location/Qualifiers
 XX FT 2034..2774
 XX FT CDS /*tag= a
 FT /product= "osmotin"
 XX /transl_except= [pos:2574..2576,aa:Arg]

XX PN US5801028-A.

XX XX 01-SEP-1998.

XX PD 07-JUN-1995; 95US-00482037.

XX PF 20-MAY-1993; 93US-00065147.

XX PR 12-JAN-1994; 94US-00180428.

XX PA (PURD) PURDUE RES FOUND.

XX PI Hasegawa EM, Bressan R;

XX DR WPI; 1998-494773/42.

XX DR P-PSDB; AAW69751.

XX PT Inhibition of pathogens in plants by recombinant expression of pathogen
 PT inhibiting proteins - uses nucleic acid constructs containing the
 PT pathogen-inhibiting proteins under control of osmotin promoter, which is
 PT inducible by specific signals.

XX PS Claim 1; Col 29-34; 26pp; English.

XX CC A method has been developed of inhibiting a pathogen in a plant. The
 CC method comprises: (a) providing or constructing a vector comprising an
 CC osmotin promoter and foreign DNA sequence encoding a pathogen-inhibiting
 CC protein, where the promoter is operably linked to the foreign DNA
 CC sequence and includes: (i) nucleotide sequence 5' of the osmotin coding
 CC sequence extending to position -248 bases from the start of the osmotin
 CC protein coding sequence, the coding sequence defined as starting at bp
 CC 2034 of the 3033 bp osmotin sequence (present sequence), (ii) a
 CC nucleotide sequence which hybridizes to (i) and promotes expression of an
 CC operably linked coding sequence under conditions of desiccation; and (b)
 CC introducing the vector into the plant to create a transformed plant,
 CC where expression of the pathogen-inhibiting protein in the transformed
 CC plant is regulated by the osmotin promoter. The method is useful for the
 CC production of recombinant plants having genes under control of an osmotin
 CC promoter, especially of pathogen-inhibiting proteins. Osmotins are
 CC cationic plant proteins, similar to tobacco PR-5-type proteins. The
 CC osmotin genes are under control of hormonal or environmental signals,
 CC including abscisic acid, ethylene, tobacco mosaic virus invention,
 CC salinity, desiccation and wounding. The present sequence represents the
 CC Nicotiana tabacum osmotin gene with promoter

XX SQ Sequence 3033 BP; 973 A; 505 C; 547 G; 1008 T; 0 U; 0 Other;

Query Match 29.3%; Score 468.8; DB 2; Length 3033;
 Best Local Similarity 76.8%; Pred. No. 5.6e-95;
 Matches 679; Conservative 0; Mismatches 162; Indels 43; Gaps 7;
 QY 46 GGTATCTTTCTTTGAAAAAATTCGAAAGAACCTAGAGACACATGACCTTGGTGGTCAAC 105
 Db 2622 GGCATCTTTCTTTGAAAAAATTCGAAAGAACCTAGAGACACATGACCTTGGTGGTCAAC 2563
 QY 106 AATATTGTTCTCTCCAAATGCTTACAAAGGATTGTTACATCTCTCGGGTACTTTAAGCT 165
 Db 2562 AATATTGTTCTCTCCGAATGATACAGGGTTATTACATCTCTCGGGAACCTAAGTT 2503
 QY 166 GACTAGACATTCAACATTATATTTCGGTGCATTAATTTGTTGTCATTTCCCTCCAC 225
 Db 2502 CGCGGGGACATTCGCGCTTTATATTAGCGGTACAAATGAATTCATGGCATTTCCCTCCAC 2443
 QY 226 TTGGATTAGTCGGGGCGAAGTTCATCGGTATATTAATCAATCACTAAGAAATCTCC 285
 Db 2442 TAGGGTTAGTCGGGGCGAAGTTCATCGGAATGTTGAATCCATCACTAAGAAATCTCC 2383
 QY 286 AGAAATCTAAGTTGTTGAATGCTGCTCAAGGCGTACTCGGCTAGGGTGTGTTGGTGTTC 345
 Db 2382 AGAAATCTAAACCACTGAATTTGTTGTCGCAAGGTATTTCAGCAAGGTGTTGGTGGTTAC 2323
 QY 346 CCCACCGGTGCACTCGAGACACACCAATCACAGTATGACAGAACCTCTACAG 405
 Db 2322 CCCACCGGTGCACTCGAGACACACCAATCACAGTATGACAGAACCTCTACAG 2263
 QY 406 CACCACCGAAGTTACATCCAGTACGACCCCATATAGTGCCTAGTGCCTAGGCG 465
 Db 2262 CAGCATTAAGTTACAAATTAGTACGGCCCATACACATGTCCTTTAGTACCTCTGGCG 2203
 QY 466 CATCAATGACCCACATTGCGCTCGATCGAGACGTGCGGACCGCTATCGG-GTCCATG 524
 Db 2202 CATTGATCACCAAGTTTGGCTCGATCGAGACCGCGGACCGCTATGGGTGTGCGACG 2143
 QY 525 CGGCCCAAGCATGTATGACAGCTTGTGCGGTACTCTCGATAGTGCAGACATAAGTGA 584
 Db 2142 CCGCCCAAGCATGTATGACAGCTTGTGCGGTACTCTCGATAGTGCAGACATAAGTGA 2085
 QY 585 AGTCACAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTGTTGA 644
 Db 2084 AGTCACAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAGTTGCCCATGTTGTTGA 2025
 QY 645 AATTATATGTGACAAATATTTTGGTACT-----TTATATATA 685
 Db 2024 CATTTTTTAAACAGTTGGTGTGATATAGTGACAAATGTTTGTAGTGGTTTATATA 1965
 QY 686 GGGATATGGCGCTTTTGGCACTTACGGATATTAAATCGTATTATATAACAATATCATCTT 745
 Db 1964 GGGGAATGGCGCTTTTTCGTACTATGATATTAATC-----ATAATATTATTACATT 1910
 QY 746 TGACTAATTATAACGAATATATATTAACAATATGATTTGGTAAACGTTGAGGTGG-AAAAA 804
 Db 1909 TGAATA---ATAACGGATATATCTCAAGGATGCTTTGGCAAGATGAGAGGGCGGCTTA 1853
 QY 805 TGTATAGAGCGCCCTTAATTAATTTATTTATGAATATAGCTATAGTACAACTTAA 864
 Db 1852 ACATTAAGAGCGCCCTTAATTAATTTATTTATGAATATAG-----AAGTCA 1805
 QY 865 CTTTATTGGTGATAACTTTGACATATAAATCTCTGTACGTGAC 908
 Db 1804 ATTTATTGGTAATACCGTGCCTATATAATCTCTGTACGTGAC 1761

RESULT 5

AAK16340/c

ID AAK16340 standard; DNA; 3033 BP.

XX AC AAK16340;

XX DT 26-APR-1999 (first entry)

PS Claim 18; Page 17; 25pp; English.

XX The full-length cDNA clone encoding antifungal protein AP20 was obtained from a lambda ZAP cDNA library prepared from tobacco mosaic virus-infected Samsun NH tobacco leaves. The library was screened with a probe for sequences homologous to the NP24 gene of tomato. One positive clone was found to contain the complete coding sequence for osmotin except for the A-T dinucleotide of the translation initiation codon. With the use of PCR, a BamHI site and an A-T dinucleotide was introduced in front of the osmotin cDNA; behind the gene a BamHI site was introduced. See also CC AAQ15270. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 883 BP; 220 A; 198 C; 205 G; 260 T; 0 U; 0 Other;

Query Match 26.3%; Score 419.8; DB 2; Length 883;
 Best Local Similarity 84.0%; Pred. No. 3.8e-84;
 Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAATTTGAAAAAGAGCTAGGACCATGAGCTTGGGTGCAAC 105
 DB |||||
 QY 605 GGCATCTTTGTTGAAAAATTTTGAAAAATTTAGAAAAATTTAGAACATCTCTTGTGTCAC 546
 DB |||||
 QY 106 AATATGTTGCTCCCAATGTTGACAAAGATGTTATCATCTCTCCGGTACTTTAAGCT 165
 DB |||||
 QY 545 AATATGTTGCTCCCAATGTTGACAAAGATGTTATCATCTCTCCGGTACTTTAAGCT 486
 DB |||||
 QY 166 GACTAGGACATTCACCATTTATATTTGCGCTGATGATGTTGGCATTTCCCTCCAC 225
 DB |||||
 QY 485 CGCGGGGACATTCGCGGTTTATATTAGCGGTACATGAATTCATGCGCATTTCCCTCCAC 426
 DB |||||
 QY 226 TTGGATTAGTCGGGCGAAAGTCATCGGTATATTAAATCATCACTAAGAAATGTCC 285
 DB |||||
 QY 425 TAGGGTTAGTCGGGCGAAAGTCATCGGTATATTAAATCATCACTAAGAAATGTCC 366
 DB |||||
 QY 286 AGAATCTAAACCATGAAATTTGAAAAATTTTGAAAAATTTAGAACATCTCTTGTGTCAC 345
 DB |||||
 QY 365 GGCATCTTTGTTGAAAAATTTTGAAAAATTTAGAAAAATTTAGAACATCTCTTGTGTCAC 306
 DB |||||
 QY 346 CCCACCGGTGACACTGACGAGACACCAACCAATTCACAGTATGACGAACTTACCAG 405
 DB |||||
 QY 305 CCCACCGGTGACACTGACGAGACACCAACCAATTCACAGTATGACGAACTTACCAG 246
 DB |||||
 QY 406 CACACCGGTGACACTGACGAGACACCAACCAATTCACAGTATGACGAACTTACCAG 465
 DB |||||
 QY 245 CACATTAAGTTTACCAATTTAGTACGCGCCCATACACGTCCTTTTAGTACCTCTGCGG 186
 DB |||||
 QY 466 CATCAATGACCCACATTTGGCTTCGATCGAGAGCTGCGGACCGCTATCGG-GTCCATG 524
 DB |||||
 QY 185 CATTAATGACCCCAAGTTTGGCTTCGATCGAGAGCTGCGGACCGCTATCGG-GTCCATG 126
 DB |||||
 QY 525 CGGCCCAACCGGTGACGAGACACCAACCAATTCACAGTATGACGAACTTACCAG 584
 DB |||||
 QY 125 CGGCCCAACCGGTGACGAGACACCAACCAATTCACAGTATGACGAACTTACCAG 68
 DB |||||
 QY 585 AGTCACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 637
 DB |||||
 QY 67 AGTCACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15

RESULT 7
 AAQ15270/c
 ID AAQ15270 standard; DNA; 884 BP.
 XX AAQ15270;
 AC
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 16-MAR-1992 (first entry)
 XX
 XX
 DE Encodes C-terminally truncated osmotin-like antifungal protein.
 XX tobacco; osmotic tolerance; AP20; ss.
 XX
 XX
 OS Nicotiana tabacum.

XX Key Location/Qualifiers
 CDS 17..694
 FT /*tag= a
 FT /note= "secretable osmotin-like protein"
 XX
 XX EP460753-A.
 XX
 XX 11-DEC-1991.
 XX
 XX 31-MAY-1991; 91EP-00201344.
 XX
 XX 07-JUN-1990; 90NL-00001293.
 XX (MOGE-) MOGEN INT NV.
 XX Woloshuk CP, Melchers LS, Cornelisse BJ, Meulenhoff EJ;
 XX Selabuurla MB, Vandenelze PJ;
 XX WPI: 1991-363235/50.
 XX P-PSDB; AAR15661.
 XX
 XX New antipathogenic proteins obtd. from plants - obtd. by inducing
 XX resistance in plant to pathogen and prepn. of extract from plant.
 XX
 XX Claim 18; Page 19; 25pp; English.
 XX
 XX The full-length cDNA clone encoding antifungal protein AP20 was obtained from a lambda ZAP cDNA library prepared from tobacco mosaic virus-infected Samsun NH tobacco leaves (see AAQ15269). To allow secretion of the protein into the extracellular space, a T residue was inserted between nucleotides 694 and 695 of AAQ15269. This introduces a STOP codon. The mutated cDNA thus encodes an osmotin lacking the 20 C-terminal amino acids of the wild-type osmotin and which is targeted extracellularly. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 884 BP; 220 A; 198 C; 205 G; 261 T; 0 U; 0 Other;

Query Match 26.3%; Score 419.8; DB 2; Length 884;
 Best Local Similarity 84.0%; Pred. No. 3.8e-84;
 Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAATTTGAAAAAGAGCTAGGACCATGAGCTTGGGTGCAAC 105
 DB |||||
 QY 605 GGCATCTTTGTTGAAAAATTTTGAAAAATTTAGAAAAATTTAGAACATCTCTTGTGTCAC 546
 DB |||||
 QY 106 AATATGTTGCTCCCAATGTTGACAAAGATGTTATCATCTCTCCGGTACTTTAAGCT 165
 DB |||||
 QY 545 AATATGTTGCTCCCAATGTTGACAAAGATGTTATCATCTCTCCGGTACTTTAAGCT 486
 DB |||||
 QY 166 GACTAGGACATTCACCATTTATATTTGCGCTGATGATGTTGGCATTTCCCTCCAC 225
 DB |||||
 QY 485 CGCGGGGACATTCGCGGTTTATATTAGCGGTACATGAATTCATGCGCATTTCCCTCCAC 426
 DB |||||
 QY 226 TTGGATTAGTCGGGCGAAAGTCATCGGTATATTAAATCATCACTAAGAAATGTCC 285
 DB |||||
 QY 425 TAGGGTTAGTCGGGCGAAAGTCATCGGTATATTAAATCATCACTAAGAAATGTCC 366
 DB |||||
 QY 286 AGAATCTAAACCATGAAATTTGAAAAATTTTGAAAAATTTAGAACATCTCTTGTGTCAC 345
 DB |||||
 QY 365 GGCATCTTTGTTGAAAAATTTTGAAAAATTTAGAAAAATTTAGAACATCTCTTGTGTCAC 306
 DB |||||
 QY 346 CCCACCGGTGACACTGACGAGACACCAACCAATTCACAGTATGACGAACTTACCAG 405
 DB |||||
 QY 305 CCCACCGGTGACACTGACGAGACACCAACCAATTCACAGTATGACGAACTTACCAG 246
 DB |||||
 QY 406 CACACCGGTGACACTGACGAGACACCAACCAATTCACAGTATGACGAACTTACCAG 465
 DB |||||
 QY 245 CACATTAAGTTTACCAATTTAGTACGCGCCCATACACGTCCTTTTAGTACCTCTGCGG 186
 DB |||||
 QY 466 CATCAATGACCCACATTTGGCTTCGATCGAGAGCTGCGGACCGCTATCGG-GTCCATG 524
 DB |||||
 QY 185 CATTAATGACCCCAAGTTTGGCTTCGATCGAGAGCTGCGGACCGCTATCGG-GTCCATG 126
 DB |||||
 QY 525 CGGCCCAACCGGTGACGAGACACCAACCAATTCACAGTATGACGAACTTACCAG 584
 DB |||||
 QY 125 CGGCCCAACCGGTGACGAGACACCAACCAATTCACAGTATGACGAACTTACCAG 68
 DB |||||
 QY 585 AGTCACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 637
 DB |||||
 QY 67 AGTCACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15

QY 525 CGCCCAACGATGATGGACAGTTGTTGGCGGTACCTCGATAGTGACAGCATAAGTGAA 584
 DB 125 CGCCCAACGATGATGGACAGTTGTT--TCGGACCTCGATAGTGACAGCATAAGTATA 68
 QY 585 AGTCACAAAGCCGAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 637
 DB 67 AGTCACAAAGCCGAGAGGAGAAACCAAAAGAGATCTCAAGTTGCCCATGT 15
 RESULT 8
 ID AAV68641/c
 AC AAV68641 standard; DNA; 741 BP.
 XX
 XX AAV68641;
 DT 12-MAR-1999 (first entry)
 DE Nucleotide sequence of the osmotin AP24.
 XX
 XX Osmotin AP24; beta-(1,6)-glucanase; bG; chimeric DNA;
 KW anti-fungal composition; transgenic plant; pathogen resistant; ds.
 XX
 XX Nicotiana tabacum.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..741
 FT /*tag= a
 FT /product= "osmotin AP24"
 XX
 PN WO9849331-A1.
 XX
 XX 05-NOV-1998.
 PD
 XX 27-APR-1998; 98WO-EP002560.
 PF
 XX 29-APR-1997; 97EP-00201254.
 PR
 XX (MOGE-) MOGEN INT NV.
 PA
 XX
 PI Stuiver MH, Lageweg W, Van Deventer- Troost JPE, Custers JHHV;
 DR WPI; 1999-024066/02.
 DR P-PSDB; AAW80986.
 XX
 PT Isolated protein with beta-glucanase activity - is isolated from edible
 PT fungus and used to produce pathogen resistant plants.
 XX
 PS Claim 13; Page 27-28; 47pp; English.
 XX
 CC This is the nucleotide sequence encoding the Nicotiana tabacum osmotin
 CC AP24, used in the method of the invention in conjunction with beta-(1,6)-
 CC glucanase (bG) to produce a chimeric DNA. Osmotin AP24 and beta-(1,6)-
 CC glucanase (bG) can be used in an anti-fungal composition. The chimeric
 CC DNA sequences can be transferred into plants to make them pathogen
 CC resistant
 CC
 SQ Sequence 741 BP; 182 A; 173 C; 178 G; 208 T; 0 U; 0 Other;
 Query Match 26.1%; Score 417.8; DB 2; Length 741;
 Best Local Similarity 83.9%; Pred. No. 1e-83; Gaps 2;
 Matches 496; Conservative 0; Mismatches 92; Indels 3; Gaps 2;
 QY 46 GGTATCTTTGTTGAAAGAAATGGAAGAACGTAGGACACACATGGACCTTGGGTGCAAC 105
 DB 589 GGCATCTTTGTTGAAAGAAATTTGAGAAATGTAGGACACACAGGTCTTGTGTGCAAC 530
 QY 106 AATATTGTTGCTCCCAATGTGTACAGATGTTACATCTCCGGGTACTTTAAGCT 165
 DB 529 AATATTGTTGCTCCCAATGTGTACAGATGTTAATACATCTCCGGGAACCTTAAGTT 470
 QY 166 GACTAGGACATTCACCATTTATATTGCGGTGCAATGATGTTGTCATTTCCCTCCAC 225

DB 469 CCGCGGGACATTTCGCCGTTTATTATTAGCCGTACAAATGAATTCATGGCATTTCCCTCCAC 410
 QY 226 TTGGATTAGTCGGGCGGAAAGATCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCC 285
 DB 409 TAGGGTTAGTCGGGCGGAAAGATCATCGGAATGTTGAATCCATCAACTAAAGAAATGTCCC 350
 QY 286 AGAAATCTAAAGTTGTTGAACTGGTCCAAAGGCGTACTCGGCTAGGGTGTGTTGGTGTGTC 345
 DB 349 AGAAATCTAAACCACTGAATTGGTCCAAAGCGTATTCAGCCCAAGGTGTTGGTGTGTTAC 290
 QY 346 CCCACCCGTCGTCAGTCAGGACACCAATCACCAGTATGCACGAACCTCTTACCAG 405
 DB 289 CCCACCCGTCGTCAGTAGGACTCCACCACAGTACCGGTTTGGCAGCTACCCCTACCAG 230
 QY 406 CACCACCGAAGTTACATCCAGTACGACCCCAATACATACGTGCGCATCGTAGTGCCTTAGGCG 465
 DB 229 CAGCATTTGAAGTTACAAATTAGTACGGCCCAATACACGTGCCATTTTAGTACCTCGTGGCG 170
 QY 466 CATCAATGACCCACATTTGGGCTCGATCGAGACGTCGGGCGACCGCTATCGG-GTCGATG 524
 DB 169 CATTGATCACCACAGTTTGGGCTCGATCGAGCGCGCGCCGCTATGGTGTGTCGACG 110
 QY 525 CGGCCCAACGATGTATGGACAGTTGTTGGCGGTACCTCGATAGTGACAGCATAAAGTAA 584
 DB 109 CGGCCCAACGCGGTACGGACAGTTGTT--TCGGACCTCGATAGTGGCAGCATAAAGTATA 52
 QY 585 AGTCACAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCAT 635
 DB 51 AGTCACAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAGTTGCCCAT 1
 RESULT 9
 ID AAQ21414/c
 AC AAQ21414 standard; DNA; 1004 BP.
 XX
 XX AAQ21414;
 DT 10-JUN-1992 (first entry)
 DE Encodes osmotin-like protein from tobacco plant.
 XX
 KW drought tolerance; salt tolerance; environmental stress; ss.
 XX Nicotiana tabacum.
 FH Key Location/Qualifiers
 FT sig_peptide 18..80
 FT /*tag= a
 FT mat_peptide 81..773
 FT /*tag= b
 FT /product= "osmotin_like_protein"
 XX
 PN JP04018099-A.
 PD 22-JAN-1992.
 XX
 XX 10-MAY-1990; 90JP-00121816.
 XX 10-MAY-1990; 90JP-00121816.
 XX (NAGS) NAGASE SANGYO KK.
 PA WPI; 1992-075255/10.
 XX P-PSDB; AAR21426.
 DR
 XX Amino-acid sequence for protein resembling osmotic - for prodn. of higher
 PT plants resistant to stress such as drought, salt etc.
 PT
 XX Claim 3; Fig 1; 10pp; Japanese.
 PS
 CC The protein encoded by this DNA is an osmotin-like protein involved in
 CC resistance to stress in higher plants. Stress may be caused by e.g. viral
 CC infection, drought, high salt concentration, etc. See also AAQ21415-8.

XX SQ Sequence 1004 BP; 288 A; 200 C; 211 G; 305 T; 0 U; 0 Other;

Query Match 22.2%; Score 355; DB 2; Length 1004;
Best Local Similarity 76.5%; Pred. No. 1.2e-69;
Matches 461; Conservative 0; Mismatches 140; Indels 2; Gaps 2;

QY 49 ATCTTTGTTTGA AAAAATTTGGAAAGAACAGTAGACACCATGTAGACCATGTGGTGCAACAAT 108
DB 606 ATCTTTGTTTGA AACCATCTTTGATAACTCAGTAGACACCATGTGGTGCAACAAT 547

QY 109 ATTGTTGTCCTCCAAAATGTGTCAAGGATTGTACATCTCCGGGTACTTTTAAGCTGAC 168
DB 546 ATTGTTGTCCTCCAAAATGTGTACATGGTGTGTACATCTCCAGGTACCTTAAGTGAAC 487

QY 169 TAGACAACTTACCATTATATTTCCCGTGCAATGGAATGTGTGCATTTCCCTCCACTTG 228
DB 486 CAGGGCAATTCACCAATTTATGTGTGCTGTGCAATTCGGTGACATTTCCAGGACCG 427

QY 229 GATTAGTCGGGCGAAAGTCATCGGTATATTAATTCATCAACTAAAGAATGTCCCAGA 288
DB 426 GCTTAGTCGGGCCAAAAGACATAGGAATGTAATCCATCAATTACAGATGTCCACGA 367

QY 289 AATCTAAGTTGTGA ACTGTGTCGAAGCGCTACTCGGTAGGGTGTGGTGGTGGCCCC 348
DB 366 AATCTAAGTTGCTGA ATTGGTTCAAOCGTATTTCGGCTAAGGTATTTGGTGGTTACCCC 307

QY 349 ACCGGTGCACTGCAGGACACCCACCAATCACCAAGTCATGCACGACCTCTACCAGCAC 408
DB 306 ATCTTTTGCATTTCTAAGACTTTCACCAATCACCGGTTTGGCACCAACCTCTACCAGCAC 247

QY 409 CACCGAAGTTACATCCAGTACGACCCCATATACGTGCATCTAGTGCCTCCCTAGCGGCAT 468
DB 246 CATCAAAAGTTGCAATTAGTACGACCCCATATACGTGCCATTTTAGTACCAAGTGGTGC 187

QY 469 CAATGACCCACATTTGGCCCTCGATCGAGACGTGGGACCGCCTA-TCGGGTCGATGCCG 527
DB 186 AGAACACCAACTTTGACCTCGTTCGAGACGTGGGCCACGCGCTACAGGGGTTGCCGCTG 127

QY 528 CCCAAACGATGTATGGACAGTTGTT-GCCGGTACTCTCGATAGTGACAGCATAAGTGAAG 586
DB 126 CCCAGCGGTGTATGGGCAATTGTTATGGACTTCAATACGCCGAAGCATATAGTATAAG 67

QY 587 TCACAAAGCCAGAGGAGGAAACCAAAAGAACTCAAGTAGCCCATGTTTTTTGAAA 646
DB 66 TCACAAAGGCAAGGAGGAAGAACTAAAAAAGTTGTCAAGTGAAGTCAATTTAGTGGACT 7

QY 647 TTT 649
DB 6 TTT 4

RESULT 10
AAC47993/c
ID AAC47993 standard; DNA; 906 BP.
AC AAC47993;
XX AC
XX DX
XX DT
XX DE
XX DE
XX DE
XX KW
XX KW
XX KW
XX OS
XX PN
XX PD
XX PF

18-OCT-2000 (first entry)
Arabidopsis thaliana DNA fragment SEQ ID NO: 55872.
Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway; metabolic pathway;
promoter; termination sequence; ss.
Arabidopsis thaliana.
EPI033405-A2.
06-SEP-2000.
25-FEB-2000; 2000EP-00301439.


```
Db      150 TCGCGCAGCCACACGGTGTAACTACATTGTT--TAGGATTTCGAATGTGGCGCGTGT 93
Qy      580 GTGAAGTCAAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCAAGTTT 639
Db      92  GCGGTGGAGATGAGCAAAAGTGGCGMAATATGAAGTAGAGACCAAGAGGTTTGCCATT 33
Qy      640 GTTGAATTTA 650
Db      32  TTTTAGTTCTA 22

RESULT 11
ID AAC47227/c
XX AAC47227 standard; DNA; 902 BP.
XX AC AAC47227;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 53029.
XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX FN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123189P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 28-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147600P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
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PR	09-AUG-1999;	99US-0147933P.	Db	615	GGCATCTCTGCTTAAAGAAATCTTGAGTACTCAGTATCGCTACATGATCCCTGACGTTTCG	556
PR	10-AUG-1999;	99US-0148171P.	QY	100	TGCACAAATATTGTTGCTCTCCAAATGTGTACAAAGATTGTTTATCATCTCTCGGGTACTTT	159
PR	11-AUG-1999;	99US-0148319P.	Db	555	TACACAGTATTGTTGCTCTGAAATACAGTACACGGGTGTTGTCATCCACTCGGGCTC	496
PR	12-AUG-1999;	99US-0148341P.	QY	160	TAAGCTGACTAGACATTCACCAATTTATTTCCCGTGCATTTGAATTTGTGGCATTTC	219
PR	13-AUG-1999;	99US-0148565P.	Db	495	TCACACAGTTTGGACATTTGCTCGTTTATGTTCTGCGGTACATAGTATCCGATGGCAGTTC-	437
PR	17-AUG-1999;	99US-0149175P.	QY	220	CTCCACTTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCACTAAAGAAA	279
PR	18-AUG-1999;	99US-0149428P.	Db	436	-----GAACTAGTTGGCTAAACTCCATAGGTATGTTAAATCCATCGACAGTGAGA	385
PR	20-AUG-1999;	99US-0149722P.	QY	280	TCTCCAGAAATCTAAGTTGTTGAATCGTCCAGCGCTACTCGGCTAGGTTGTTGGTG	339
PR	27-AUG-1999;	99US-0151065P.	Db	384	TATCGTAGAAGTCTAAGTTGTTGAATTTGGTTCAAAGCGTACTCAGCCAAACGTTTGGTG	325
PR	27-AUG-1999;	99US-0151066P.	QY	340	GTTTGCCTCCACCGCTGCACTGCAGGACACACCAATCCAGTCACTGACGACGACCTC	399
PR	27-AUG-1999;	99US-0151067P.	Db	324	GCTGTCCCGCAGTACATTGGAGTCCACCTGCACTGCACTGCACTGCACTGCACTGCACTG	265
PR	30-AUG-1999;	99US-0151303P.	QY	400	TACAGCACACCGAAGTTACATCCAGTACGACCCCATATATCGTGCCATCGTAGTGC	459
PR	31-AUG-1999;	99US-0151438P.	Db	264	GACCTGAGGAGTCAAAGTTTACAATTTGGTCTTACCCCAATCCGTTGCTGCTGCTGCTG	205
PR	01-SEP-1999;	99US-0151930P.	QY	460	TAGGCGCATCATGACCCACATTTGGCTTCGATCGAGACGTCGGGCGACCGCTATCGGT	519
PR	07-SEP-1999;	99US-0152363P.	Db	204	CCGCGACATCTAGCCTCCATGATTGGCCAGCATCTAGACGTCGGCCACTCC--AGGCGT	147
PR	13-SEP-1999;	99US-0153070P.	QY	520	CGATGCCGCCCAACGATGTATGACAGTGTGTGGCGGTACTGCGGTACTGATAGTGACAGCATAA	579
PR	15-SEP-1999;	99US-0154018P.	Db	146	TGCGCGACGCCACACGCGTGAACATTTGTT--TAGGATTTCAATGTGCGCGCTGTT	89
PR	16-SEP-1999;	99US-0154039P.	QY	580	GTGAAAGTCAAAAGCCAGAGGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTT	639
PR	20-SEP-1999;	99US-0154779P.	Db	88	GCGGTGGAGATGAGCAAAAGTCCGAAATATGAAAGTAGAGACCAAGAGGTTTGGCAATT	29
PR	22-SEP-1999;	99US-0155113P.	QY	640	GTTGAAATTTA	650
PR	23-SEP-1999;	99US-0155486P.	Db	28	TTTATGTTCTA	18
PR	24-SEP-1999;	99US-0155659P.	RESULT 12			
PR	29-SEP-1999;	99US-0156458P.	ABZ14313/c			
PR	04-OCT-1999;	99US-0157117P.	ID	ABZ14313	standard; DNA; 735 BP.	
PR	05-OCT-1999;	99US-0157753P.	XX	ABZ14313;		
PR	06-OCT-1999;	99US-0157855P.	AC	ABZ14313;		
PR	07-OCT-1999;	99US-0158029P.	XX	21-JAN-2003	(first entry)	
PR	08-OCT-1999;	99US-0158232P.	DT	21-JAN-2003	(first entry)	
PR	12-OCT-1999;	99US-0158232P.	XX	Arabidopsis thaliana	stress regulated gene SEQ ID NO 2118.	
PR	13-OCT-1999;	99US-0159293P.	DE	Arabidopsis thaliana	stress regulated gene SEQ ID NO 2118.	
PR	13-OCT-1999;	99US-0159293P.	XX	Arabidopsis thaliana	plant; gene; stress; transgenic; ds.	
PR	13-OCT-1999;	99US-0159293P.	KW	Arabidopsis thaliana		
PR	14-OCT-1999;	99US-0159329P.	XX	Arabidopsis thaliana		
PR	14-OCT-1999;	99US-0159330P.	OS	Arabidopsis thaliana		
PR	14-OCT-1999;	99US-0159331P.	XX	WO200216655-A2.		
PR	14-OCT-1999;	99US-0159637P.	FN	28-FEB-2002.		
PR	14-OCT-1999;	99US-0159638P.	XX	24-AUG-2001;	2001WO-US026685.	
PR	21-OCT-1999;	99US-0160741P.	PD	24-AUG-2000;	2000US-0227866P.	
PR	21-OCT-1999;	99US-0160767P.	XX	26-JAN-2001;	2001US-0264647P.	
PR	21-OCT-1999;	99US-0160767P.	XX	22-JUN-2001;	2001US-0300111P.	
PR	21-OCT-1999;	99US-0160788P.	XX	(SCRI) SCRIPPS RES INST.		
PR	21-OCT-1999;	99US-0160770P.	XX	(SYGN) SYNGENTA PARTICIPATIONS AG.		
PR	21-OCT-1999;	99US-0160814P.	XX	Harper JF, Kreps J, Wang X, Zhu T;		
PR	21-OCT-1999;	99US-0160815P.	XX			
PR	22-OCT-1999;	99US-0160980P.	XX			
PR	22-OCT-1999;	99US-0160981P.	XX			
PR	22-OCT-1999;	99US-0160989P.	XX			
PR	25-OCT-1999;	99US-0161404P.	XX			
PR	25-OCT-1999;	99US-0161405P.	XX			
PR	25-OCT-1999;	99US-0161406P.	XX			
PR	26-OCT-1999;	99US-0161359P.	XX			
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PR	26-OCT-1999;	99US-0161361P.	XX			
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PR	28-OCT-1999;	99US-0161922P.	XX			
PR	28-OCT-1999;	99US-0161993P.	XX			
PR	29-OCT-1999;	99US-0162142P.	XX			
PR	29-OCT-1999;	99US-0162142P.	XX			

Query Match 11.7%; Score 187.4; DB 3; Length 902;
 Best Local Similarity 61.5%; Pred. No. 4e-32;
 Matches 376; Conservative 0; Mismatches 216; Indels 19; Gaps 4;

XX	27-FEB-2003	(first entry)	
XX	DT		
XX	DE	Arabidopsis thaliana gene #80 modulated by PTGS.	
XX	KW	Posttranscriptional gene silencing; PTGS; plant; transformation; gene;	
XX	XX	ss.	
XX	OS	Arabidopsis thaliana.	
XX	Key	Location/Qualifiers	
XX	FT	1..735	
XX	CDS	/*tag= a	
XX	FN	WO200281695-A2..	
XX	XX		
XX	PD	17-OCT-2002.	
XX	PF	05-APR-2002; 2002WO-EP003806.	
XX	PR	06-APR-2001; 2001US-0282049P.	
XX	XX	(SYGN) SYNGENTA PARTICIPATIONS AG.	
XX	PA	(FRIE-) FRIEDRICH MIESCHER INST.	
XX	XX		
XX	PI	Zhu T, Glazov EA, Meins F, Wang X, Chang H;	
XX	XX		
XX	WPI	2003-103337/09.	
XX	DR	P-FSDE; ABP81252.	
XX	XX		
XX	PT	Novel polynucleic acid segment useful for modulating gene expression	
XX	PT	within a cell by posttranscriptional gene silencing, and for augmenting a	
XX	PT	plant cell genome.	
XX	PS	Claim 19; Page 324-325; 438pp; English.	
XX	CC	The invention relates to a novel isolated polynucleic acid segment	
XX	CC	modulated within a cell by posttranscriptional gene silencing (PTGS). The	
XX	CC	invention specifically relates to a method to identify an expression	
XX	CC	product that is modulated by PTGS. The polynucleotide is useful for	
XX	CC	modulating the gene expression within a cell by PTGS, by introducing the	
XX	CC	polynucleic acid into a cell and expressing the nucleic acid segment in	
XX	CC	the cell to form a product. The polynucleic acid segment is also useful	
XX	CC	for augmenting a cell genome, and for augmenting a plant genome, by	
XX	CC	contacting a plant cell with the segment to produce a transformed plant	
XX	CC	cell, and growing the transformed plant cell to produce a differentiated	
XX	CC	transformed plant. The sequences shown in AB242017 - AB242142 represent	
XX	CC	segments of A. thaliana cDNA modulated by PTGS	
XX	SQ	Sequence 735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;	
	Query Match	11.7%; Score 186.8; DB 7; Length 735;	
	Best Local Similarity	62.4%; Pred.No. 5.2e-32;	
	Matches 367; Conservative	0; Mismatches 202; Indels 19; Gaps 4	
QY	46	GGTATCTTTGTTGAAAAAATTGAAAAAGAACGTAGACCAATG-----GACCTGGG 99	
DB	586	GGCATCTCTGTTTAAAGAATTCTGAGTACTGCTATCGTATCGGTATCCCTGACCGTTGG 527	
QY	100	TGCAACAATATTGTTGCTCTCCAATTGGGTACAAGATTGTTACATCTCCGGGTACTTT 159	
DB	526	TACACAGTATTGGTTCGTCGTAATACAGTACACGGTGTGTGCATCCACCTGGGCTC 467	
QY	160	TAACTGATAGGACATTCACCATTTATATTGCGGTGCATGAAATGTGTGGCATTTCC 219	
DB	466	TCACACCGTTTGGACATGTGCGGTTTATGTCTCGGTACATAGTATCCGATGGCATGTC- 408	
QY	220	CTCCACTTTGGAATTAGTTCGGGCGGAAGTCAATCGTATATTAAATCCATCAACTAAGAAA 279	
DB	407	-----GACTAGTTGGGCTAAACTCCATAGTATGTTAAATCCATCGACAAGTGACA 356	
QY	280	TGTCGCCAAGAAATCTAAGTTGTTGAACCTGGTCCGAAGCGGTACTCGGTAGGGTGTTTGGTG 339	

Db 355 TATCGTAGAAGTCTAAGTTGTTGAATTGGTTCAAGCGTACTAGCCAAAGTGTGTTGGT 296
 QY 340 GTTTGCCCCACCCGGTGCACATGACGAGACACCAACATCACCAGTCAATGACGAACTTC 399
 Db 295 GCTGTCCCGCCAGTACATTTGGAGTCCACCACATGACATCACCAGTTTGGCATCGGCCAC 236
 QY 400 TACCAGACACCCGAGTTATCATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCC 459
 Db 235 GACCTGAGAGTCAAAAGTTCAATTTGGTCTTACCCCAATCCGTCGCAATTTTAGTCCCG 176
 QY 460 TAGCGCATCAATGACCCACATTTGGGCTCGATCGAGACGTCGGGCGACCCCTATCGGGT 519
 Db 175 CCGGACATCTAGCTCCATGATTTGGCCAGCATCTAGACGTGGCCACCTCC--AGGGCT 118
 QY 520 CGATGCCCGCCAAACGATGATGACAGTTGTTGGCGGTACCTCGATAGTAGACAGATAA 579
 Db 117 TCGCGCAGCCACACCGGTAACTACATTTGGTT--TAGGATTTGGAATGTGGCGCTGTT 60
 QY 580 GTGAAAGTCAAAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAG 627
 Db 59 GCGGTGGAGATGACCAAAAGTGGCGAAATATGAAGTAGAGACCAAG 12

RESULT 14
 ADA68525/c
 ID ADA68525 standard; DNA; 735 BP.

XX AC ADA68525;
 XX XX
 DT 20-NOV-2003 (first entry)
 XX Arabidopsis thaliana gene, SEQ ID 566.
 DE Plant; bacterial infection; fungal infection; viral infection; ds.
 KW Arabidopsis thaliana.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX WO2003000898-A1.
 XX PD 03-JAN-2003.
 XX PF 22-JUN-2001; 2001WO-IB001105.
 XX PR 22-JUN-2001; 2001WO-IB001105.
 XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WP1; 2003-175290/17.

Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.

Claim 6; SEQ ID NO 566; 899pp; English.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to the expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

Sequence 735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;

Query Match 11.7%; Score 186.8; DB 7; Length 735;

Best Local Similarity 62.4%; Pred. No. 5.2e-32;
 Matches 367; Conservative 0; Mismatches 202; Indels 19; Gaps 4;

QY 46 GGTATCTTTTGTGAAAAAATTTGAAAAAGACGTAGGACCCACATG-----GACCTTGGG 99
 Db 586 GGCATCTCTGCTTAAAGAAATCTTGAGTACTCAGTATCGTACATGATCCCTGACCGTTGC 527
 QY 100 TGCACATATTTGTTGCTCTCCAAATGTGGTACAGAGATTGTTACATCTCCGGGTACTT 159
 Db 526 TACAACAGTATTTGTTGCTCTGTAATACAGTACAGGGTTGTTGCATCCACCTCGGGGTC 467
 QY 160 TAAGCTGACTAGGACATTCACCATTTATTTGCGTGCATTGAATTGTGGCAATTTCC 219
 Db 466 TCACACAGTTTGGACATTTGCGTTTATGTTCTGGTACATAGTATCGATGGCAGTTC- 408
 QY 220 CTCCTACTTGGATTAGTTCGGGGCGAAGTCATCGGTATATTAATCCATCAACTAAAGAAA 279
 Db 407 -----GACTAGTTGGGCTAAACTCCATAGGTATGTTAAATCCATCGCAAGTGAGA 356
 QY 280 TGTCCACAGAAATCTAAGTTGTTGAACTGCTCCAGGGGTACTCGGCTAGGGTGTGTTGGTG 339
 Db 355 TATCGTAGAAGTCTAAGTTGTTGAATTGTTCAAGCGTACTCAGCCAACTGTTTGGT 296
 QY 340 GTTTCCTCCACCCCGGTGCACTGCAGGACACCAACCAATCAATCCAGTCAATGACCAACCTC 399
 Db 295 GCTGTCCCGCCAGCCAGTACATTTGGAGTCCACCCTGACGTACCAGTTTGGCATCGGCCAC 236
 QY 400 TACCAGACACCCGAGTTATCATCCAGTACGACCCCATATACGTGCCATCGTAGTGGCCCC 459
 Db 235 GACCTGAGGAGTCAAAAGTTTCAATTTGGTCTTACCCCAATCCGTCGCAATTTAGTGCCCC 176
 QY 460 TAGGGCATCAATGACCCACATTTGGCTCGATCGAGACGTCGGGCGACCCGCTATCGGGT 519
 Db 175 CCGGACATCTAGCTCCATGATTTGGCAGCATCTAGACGTTCGGCCACCTCC--AGGGCT 118
 QY 520 CGATGCCCGCCAAACGATGATGACAGTTGTTGGCGGTACTCGATAGTAGACAGATAA 579
 Db 117 TCGCGCAGCCACACCGGTAACTACATTTGGTT--TAGGATTTGGAATGTGGCGCTGTT 60
 QY 580 GTGAAAGTCAAAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAG 627
 Db 59 GCGGTGGAGATGACCAAAAGTGGCGAAATATGAAGTAGAGACCAAG 12

RESULT 15
 ABN98566/c
 ID ABN98566 standard; DNA; 950 BP.

XX AC ABN98566;
 XX XX

DT 01-AUG-2002 (first entry)

XX Arabidopsis thaliana expressed polynucleotide SEQ ID NO 334.

XX Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
 KW disease; crop; thale cress; tolerance factor; insect; pathogen;
 XX nutrition; ds.

OS Arabidopsis thaliana.

XX US2002023281-A1.

XX 21-FEB-2002.

XX 26-JAN-2001; 2001US-00770445.

XX 27-JAN-2000; 2000US-0178472P.

XX (GORL/) GORLACH J.

XX (ANYI/) AN Y.

XX (HAM/) HAMILTON C M.

XX (PRIC/) PRICE J L.

XX (RAIN/) RAINES T M.

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100 QY TCACAACATATTGTTGCTCTCCAAATGCGTACAAAGATTGTTACATCTCTCGGGTACTT 159
101 Db TACAAACAGTATTGGTTGCTCTCGAAATAACAGTACACGGGTTGTTGTCATCCACCTCGGGCTC 475
102 QY TAAGCTGACTAGGACATTCACCATTTATTTGCGGTGCATTCAAATTTGCTGCGCATTTCC 219
103 Db TCACAACAGTTTGGACATTTGCTCGGTTATGTTCTCGGTACATAGTATCCGATGCGAGTTC- 416
104 QY CTCCTACTGGATTAGTTCGGGCGGAAGTCATCGGTATATTTAAATCCATCAACTAAAGAAA 279
105 Db GAACTAGTTGGCTTAAACTCCATAGGTATGTTAAATCCATCGACAAGTGAGA 364
106 QY TGTCTCCAGAACTTAAGTTGTTGAACGTGTTCCAGGCGGTACTCGGCTAGGGTGTGTTGGTG 339
107 Db TATCTGTAAGTCTAAGTTGTTGAAATTTGGTTTCAAAGCGTACTCAGCCACAGTGTTTGGTG 304
108 QY GTTTCGCCCCACCCCGTGCACCTGTCAGGACACACACCAATCACCAGTCACTGACGAACCTC 399
109 Db GCTGTCCCCGACCGAGTACATTGGAGTCCACCCTGCACTCACCAGTTTGGCATCGGCCAC 244
110 QY TACGAGCAGCACCAGNAGTTACATCCAGTACGAGCCCATATACGTGCCATCGTAGTGCCTCC 459
111 Db GACCTTGAGGAGTCAAAGTTACAATTTGTTCTTACCCCAATCCGTGCAATTTTAGTGCCTG 184
112 QY TAGGCGGCATCAATGACCCACACATTTTGGCTCGATCGAGACGTGCGGCGACCCGCTATCGGGT 519
113 Db CCGGACATCTAGCCTCCATGTTGGCCAGCATCTAGACGTGCGGCACCTCC--AGGGCT 156
114 QY CGATCGCGCCCMACGATGTTATGACAGTGTGTTGGCGGTACCTCGATAGTGACAGCATAA 579
115 Db TCGCGCAGCCACACGCGTGAACATACATGCGTT--TAGGATTTGCAATGTGGCGCGTGT 68
116 QY GTGAAAGTCACAAAGCCAGAGGAGAAACCAAAAGAAGATCTCAAG 627
117 Db GCGGTGGAGATGACGAAGAAGTCCGCGAAAATATGAAAGTAGAGACCAAG 20

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	Query Match	11.7%	Score 186.8;	DB 6;	Length 950;
	Best Local Similarity	62.4%;	Pred. No. 5.5e-34;		
	Matches 367;	Conservative 0;	Mismatches 202;	Indels 19;	Gaps 4;
QY	46	GGTATCTTCTTTTGA	AAAAATTG	GA	AAAGAACG
					TAGGACCCACATG-----GACCTTGGG
DB	594	GGCATCTCTGTTTAA	AGAAATCTT	TGAGTACT	CAGTATCGTACATGATCCCTGACCGTTTCG
					535

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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	468.8	29.3	3033	1	US-08-482-037A-1
C 2	419.8	26.3	883	1	US-07-828-798C-4
C 3	419.8	26.3	883	2	US-08-315-868A-4
C 4	419.8	26.3	883	3	US-08-495-819B-4
C 5	419.8	26.3	884	1	US-07-828-798C-5
C 6	419.8	26.3	884	2	US-08-315-868A-5
C 7	419.8	26.3	884	3	US-08-495-819B-5
C 8	168.8	10.6	875	4	US-09-589-733C-4
C 9	144.8	9.1	900	1	US-08-181-271A-4
C 10	144.8	9.1	900	1	US-08-449-315-4
C 11	144.8	9.1	900	1	US-08-444-803-4
C 12	144.8	9.1	900	1	US-08-449-043-4
C 13	144.8	9.1	900	1	US-08-456-265A-4
C 14	144.8	9.1	900	1	US-08-456-416-4
C 15	144.8	9.1	900	1	US-08-455-244-4
C 16	144.8	9.1	900	1	US-08-454-876-4
C 17	144.8	9.1	900	2	US-08-457-364-4
C 18	144.8	9.1	900	2	US-08-456-262-4
C 19	144.8	9.1	900	2	US-08-456-240-4
C 20	144.8	9.1	900	2	US-08-455-736-4
C 21	144.8	9.1	900	2	US-08-971-217-4
C 22	144.8	9.1	900	3	US-09-350-600-4
C 23	144.8	9.1	900	4	US-09-906-234-4
C 24	138.6	8.7	910	4	US-09-685-292-1
C 25	109	6.8	894	1	US-08-178-708-7
C 26	109	6.8	894	1	US-08-457-552-7
C 27	109	6.8	894	1	US-08-456-430-7

C 28	109	6.8	894	2	US-08-994-418-7
C 29	109	6.8	894	5	PCR-US95-00432-7
C 30	90.8	5.7	1309	6	5221624-4
C 31	90.6	5.7	621	4	US-09-224-514A-9
C 32	89.2	5.6	621	4	US-09-224-514A-1
C 33	89.2	5.6	621	6	5221624-31
C 34	81.4	5.1	624	2	US-08-426-599B-3
C 35	75.2	4.7	624	2	US-08-426-599B-1
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C 39	53.8	3.4	1924	4	US-09-424-283-5
C 40	52.6	3.3	640681	4	US-09-790-988-1
C 41	52	3.3	6583	4	US-10-204-708-25
C 42	51.4	3.2	288	4	US-09-598-401C-38
C 43	51.4	3.2	3095	6	5231168-1
C 44	49.6	3.1	6152	3	US-08-973-462-1
C 45	49.4	3.1	5152	4	US-10-204-708-74

ALIGNMENTS

RESULT 1
US-08-482-037A-1/c
; Sequence 1, Application US/08482037A
; Patent No. 5801028
; GENERAL INFORMATION:
; APPLICANT: Ray Bressan and Paul M. Hasegawa
; TITLE OF INVENTION: Osmotin Gene Promoter and Use Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas Q. Henry
; STREET: Bank One Tower, Suite 3700, 111 Monument Circle
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204-5137
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: COMPAQ
; OPERATING SYSTEM: MSDOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,037A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,243
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/180,428
; FILING DATE: January 12, 1994
; APPLICATION NUMBER: 08/065,147
; FILING DATE: May 20, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas Q. Henry
; REGISTRATION NUMBER: 28,309
; REFERENCE/DOCKET NUMBER: 7024-8/PUR16CIPDIVII
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 634-3456
; TELEFAX: (317) 637-7561
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 bases
; TYPE: Nucleotide/Amino Acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: Genomic DNA
US-08-482-037A-1
Query Match 29.3%; Score 468.8; DB 1; Length 3033;

Db 245 CAGCATTGAAGTTACAATTAGTAGCGGCCCATACACGTGCCATTTTATAGTCTCGTGGCG 186
Qy 466 CATCAATGACCCACATTTGGCTCGATCGAGACGTGCGGACCGCCTATCGG-GTCGATG 524
Db 185 CATTGATCACCAAGTTGGCTCGATCGAGACCGCGCCATATGGGTGCGACG 126
Qy 525 CCGGCCAAACGATGTATGGACAGTTGTTGGGGTACCTCGATAGTGAAGATGAA 584
Db 125 CCGGCCAAACGTTGACGACAGTTGTT--TCGGACCTCGATAGTGGCAGCATAAGTATA 68
Qy 585 AGTCACAAAAGCCAGAGGAGAACCAAAAAGAGATCTCAAGTAGCCCATGT 637
Db 67 AGTCACCAAGCAAGGAGGAAGAAACAAAGAGAGATCTCAAGTTGCCCATGT 15

RESULT 3
US-08-315-868A-4/c
; Sequence 4, Application US/08315868A
; Patent No. 5856151
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,868A
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APR-1992
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Massi, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/POCKET NUMBER: U-8622-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 883
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
US-08-315-868A-4
Query Match 26.3%; Score 419.8; DB 2; Length 883;
Best Local Similarity 84.0%; Pred. No. 6.8e-96;

Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;
Qy 46 GGTATCTTTGTTTGAATAATTTGAAAGAAAGAGAGTGGACCAATGACATGACCTTGGGTGCAAC 105
Db 605 GCACTCTTTGTTTGAATAATTTTGAATAATTTGAGAAATTTAGGACCAAGGTCTTGTGTGCAAC 546
Qy 106 AATATTTGTTGCTCTCCAAATGTGTACAAAGGATTTGTATCATCTCTCGGGTACTTTAAGT 165
Db 545 AATATTTGTTGCTCTCCAAATGTGTACAAAGGATTTGTATCATCTCTCGGGTACTTTAAGT 486
Qy 166 GACTAGGACATTCACCATTTATATTTGCGTGCATTTGAATTTGTTGGCATTTTCCCTCCAC 225
Db 485 CGCGGGGACATTCGCGGTTTATATTAGCGGTACAAATGAATTCATGGCATTTTCCCTCCAC 426
Qy 226 TTGGATTAGTCTGGGGGAAAGTCACTCGGTATATTAAATCCATCAACTAAAGAAATGTCCC 285
Db 425 TAGGGTTAGTCTGGGGGAAAGTCACTCGGTATATTAAATCCATCAACTAAAGAAATGTCCC 366
Qy 286 AGAATCTTAAGTTGTTGAATCTGTCAGAGGCGTACTCGGCTAGGTTGTTGTTGTTGCT 345
Db 365 AGAATCTTAAGTTGTTGAATCTGTCAGAGGCGTACTCGGCTAGGTTGTTGTTGTTGCT 306
Qy 346 CCCACCCGCTGCACTGCGAGGACACCAACCAATACCAAGTCAATGACGAACTTACCAG 405
Db 305 CCCACCCGCTGCACTGCGAGGACACCAACCAATACCAAGTCAATGACGAACTTACCAG 246
Qy 406 CACACCCGAGTTACATCCAGTACAGCCCATATAGTCCATCTAGTGGCCCTAGGCG 465
Db 245 CAGCATTTGAATTTACAAATTTAGTACGCGCCCATACAGTCCCATTTTAGTACCTCGTGGCG 186
Qy 466 CATCAATGACCCACATTTGGCTCGATCGAGACGTGCGGCGCCGCTATCGG-GTCGATG 524
Db 185 CATTGATCACCAAGTTTGGCTCGATCGAGACGCGGCGCCGCTATGGGTGTCGACG 126
Qy 525 CCGCCCAAACGATGTATGACAGTGTGTTGGCGGTACTCTCGATAGTGAAGATGAA 584
Db 125 CCGCCCAAACGTTGTACGGACAGTTGTT--TCGGACCTCGATAGTGGCAGCATAAGTATA 68
Qy 585 AGTCACAAAAGCCAGAGGAGAAACCAAAAAGAGATCTCAAGTAGCCCATGT 637
Db 67 AGTCACCAAGCAAGGAGGAAGAAACAAAGAGATCTCAAGTTGCCCATGT 15

RESULT 4
US-08-495-819B-4/c
; Sequence 4, Application US/08495819B
; Patent No. 6087161
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants
; TITLE OF INVENTION: with Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,819B
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APR-1992
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Massi, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/POCKET NUMBER: U-8622-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 883
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
US-08-495-819B-4
Query Match 26.3%; Score 419.8; DB 2; Length 883;
Best Local Similarity 84.0%; Pred. No. 6.8e-96;

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/315,868
; FILING DATE: 30-SEPT-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APRIL-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-010255-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-08-495-819B-4

Query Match 26.3%; Score 419.8; DB 3; Length 883;
Best Local Similarity 84.0%; Pred. No. 6.8e-96;
Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACACACATGGACCTTGGGTGCAAC 105
DB 605 GGCATCTTTGTTGAAAAAATTTGAGAAAAATGTAGGACCAAGGTCCTTGTGTGCAAC 546

QY 106 AATATTGTTGCTCCAAATGTGTGTAAGATTGTTCATCTCCGGGTACTTTAAGCT 165
DB 545 AATATTGTTGCTCCAAATGTGTGTAAGATTGTTCATCTCCGGGTACTTTAAGCT 486

QY 166 GACTAGGACATTCACCATTTATTTTCCGTTGCAATTTGAATTTGTTGGCATTTCCCTCCAC 225
DB 485 CGCGGGGACATTCGCGCTTTATTTAGCCGTACATGAATGTCATGTCATTTCCCTCCAC 426

QY 226 TTGATTAGTCGGGGCGAAAGTCATCGGTATTTAAATCCATCAACTAAAGAAATGTCCC 285
DB 425 TAGGTTAGTCGGGGCGAAAGTCATCGGTATTTAAATCCATCAACTAAAGAAATGTCCC 366

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/315,868
; FILING DATE: 30-SEPT-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APRIL-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-010255-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 883
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-08-495-819B-4

Query Match 26.3%; Score 419.8; DB 3; Length 883;
Best Local Similarity 84.0%; Pred. No. 6.8e-96;
Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACACACATGGACCTTGGGTGCAAC 105
DB 605 GGCATCTTTGTTGAAAAAATTTGAGAAAAATGTAGGACCAAGGTCCTTGTGTGCAAC 546

QY 106 AATATTGTTGCTCCAAATGTGTGTAAGATTGTTCATCTCCGGGTACTTTAAGCT 165
DB 545 AATATTGTTGCTCCAAATGTGTGTAAGATTGTTCATCTCCGGGTACTTTAAGCT 486

QY 166 GACTAGGACATTCACCATTTATTTTCCGTTGCAATTTGAATTTGTTGGCATTTCCCTCCAC 225
DB 485 CGCGGGGACATTCGCGCTTTATTTAGCCGTACATGAATGTCATGTCATTTCCCTCCAC 426

QY 226 TTGATTAGTCGGGGCGAAAGTCATCGGTATTTAAATCCATCAACTAAAGAAATGTCCC 285
DB 425 TAGGTTAGTCGGGGCGAAAGTCATCGGTATTTAAATCCATCAACTAAAGAAATGTCCC 366

QY 286 AGAAATCTAAGTTGTTGAATGTTGCCAGGCTACTCGGTAGGGTGTGTTGGTGTTCG 345
DB 365 AGAAATCTAAGTTGTTGAATGTTGCCAGGCTACTCGGTAGGGTGTGTTGGTGTTCG 306

QY 346 CCCACCCGGTGCATCTGAGGACACCAACCAATCACCAGTCATGCACGACCTTACCAG 405
DB 305 CCCACCCGGTGCATCTGAGGACACCAACCAATCACCAGTCATGCACGACCTTACCAG 246

QY 406 CACCACCGAAGTTACATCTCAGTACGACCCCATATACGTGCCATCTGAGTGCCTTAGGGG 465
DB 245 CAGCATTTGAAGTTACATTTAGTACGGCCCATACACGTCGCAATTTAGTACCTCTGGCG 186

QY 466 CATCATGACCCCATTTGGCCTCGATTCGAGAGTGTGGGACCGCCCTATCGG-GTCAATG 524
DB 185 CATGATCACCCCAAGTTTGGCCTCGATTCGAGAGTGTGGGACCGCCCTATCGG-GTCAATG 126

QY 525 CCGCCCAACGATGTATGAGCAGTTGTTGGCGGTACCTCGATAGTGACAGCATTAAGTAA 584
DB 125 CCGCCCAACGATGTATGAGCAGTTGTTGGCGGTACCTCGATAGTGACAGCATTAAGTAA 68

QY 585 AGTCACAAAAGCCGAAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 637
DB 67 AGTCACAAAAGCCGAAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 15

; US-07-828-798C-5/c
; Sequence 5, Application US/07828798C
; Patent No. 5389609
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,798C
; FILING DATE: 06-APR-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-8622-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-07-828-798C-5

Query Match 26.3%; Score 419.8; DB 1; Length 884;
Best Local Similarity 84.0%; Pred. No. 6.8e-96;
Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACACACATGGACCTTGGGTGCAAC 105
DB 605 GGCATCTTTGTTGAAAAAATTTGAGAAAAATGTAGGACCAAGGTCCTTGTGTGCAAC 546

QY 106 AATATTGTTGCTCCAAATGTGTGTAAGATTGTTCATCTCCGGGTACTTTAAGCT 165
DB 545 AATATTGTTGCTCCAAATGTGTGTAAGATTGTTCATCTCCGGGTACTTTAAGCT 486

QY 166 GACTAGGACATTCACCATTTATTTTCCGTTGCAATTTGAATTTGTTGGCATTTCCCTCCAC 225
DB 485 CGCGGGGACATTCGCGCTTTATTTAGCCGTACATGAATGTCATGTCATTTCCCTCCAC 426

QY 226 TTGATTAGTCGGGGCGAAAGTCATCGGTATTTAAATCCATCAACTAAAGAAATGTCCC 285
DB 425 TAGGTTAGTCGGGGCGAAAGTCATCGGTATTTAAATCCATCAACTAAAGAAATGTCCC 366
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; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,819B
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/315,868
; FILING DATE: 30-SEPT-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APRIL-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-010255-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-08-495-819B-5

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Query Match      26.3%; Score 419.8; DB 3; Length 884;
Best Local Similarity 84.0%; Pred. No. 6.8e-96;
Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAATTTGAAAAGACGTAGACACATGACCTTGGGTGCAAC 105
DB 605 GGCATCTTTGTTGAAAATTTGAGAAAAATGTAGACACCAAGTCTTGTGTCAAC 546
QY 106 AATATTGTTGCTCCCAATGTGTACAAGATTGTTACATCTCCGGGTACTTTAAGCT 165
DB 545 AATATTGTTGCTCCCAATGTGTACAAGATTGTTACATCTCCGGGTACTTTAAGCT 486
QY 166 GACTPAGACATTCACATTTATTTTCCCGTGATGAATTTGTGGCAATTTCCCTCCAC 225
DB 485 CGCGGGGACATTCGCGCTTATTTAGCCGTACAATGATGCAATTTCCCTCCAC 426
QY 226 TTGATTTAGTCGGGCGAAGTCACTCGGTATTTAATCCATCACTAAGAAATGTCCTC 285
DB 425 TAGGGTTAGTCGGGCGAAGTCACTCGGTATTTAATCCATCACTAAGAAATGTCCTC 366
QY 286 AGAATCTAAAGTTGTTGAACTGTGTCAGGCGTACTCGGGTAGGGTGTGTTGTTG 345
DB 365 AGAATCTAAAGTTGTTGAACTGTGTCAGGCGTACTCGGGTAGGGTGTGTTGTTG 306
QY 346 CCACCCGGTGCATGACGACACCAACCAATCAGTCATGACGAACTCTACCAAG 405
DB 305 CCACCCGGTGCATGACGACACCAACCAATCAGTCATGACGAACTCTACCAAG 246
QY 406 CACCACCGAAGTTACATCCAGTACGACCCCATATACGTGCACTGTAGTCCCTAGGG 465
DB 245 CAGCATTGAAGTTACATTTAGTACGGCCCATACAGTGCCTTTTAGTACCTCGTGG 186
QY 466 CATCAATGACCCCATTTGGCCCTCGATCGAGAGCTCGGGCACCGCCTATCGG-GT 524
DB |||||

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DB 185 CATTGATCACCCCAAGTTTGGCTCGATCGAGACGCCGCCCTATGGGTGTCAGC 126
QY 525 CCGCCCAACGATGTATGACAGTTGTTGGCGGTACCTCGATAGTACAGCATAGTGAA 584
DB 125 CCGCCCAACGGTGTACGACAGTTGTT-TGGGACCTCGATAGTGGCAGCATAGTATA 68
QY 585 AGTCACAAAGCCAGAGGAGAAACCAACCAAGAAAGATCTCAAGTAGCCCATGT 637
DB 67 AGTCACCAAGGCAAGGAGAAACCAACCAAGAAAGATCTCAAGTTGCCCATGT 15

RESULT 8
US-09-589-733C-4/c
; Sequence 4, Application US/09589733C
; Patent No. 6677503
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Craeta, Oswald R.
; APPLICANT: Duwick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; TITLE OF INVENTION: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Helianthus annuus
; US-09-589-733C-4

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Query Match      10.6%; Score 168.8; DB 4; Length 875;
Best Local Similarity 61.3%; Pred. No. 5.9e-33;
Matches 309; Conservative 0; Mismatches 187; Indels 8; Gaps 2;

QY 49 ATCTTTGTTTGAATAATTTGAAAAGAACGTAGACACATGAGACCTTGGGTGCAACAT 108
DB 577 ATCTGGCTTTGAAAACCTTGTATAATCAGTTGTTGCCAATTTCCAGAGTTGCAACAT 518
QY 109 ATTGTTGCTCCCAATGTGTACAAGATTGTTACATCTCCGGGTACTTTAAGCTGAC 168
DB 517 ACTGATCAGTTTGTACACGGTGCAGGGTTATTGACCCGCCAGAGCCCGTAACAC 458
QY 169 TAGGACATTCACATTTATTTTCCCGTGCATTAATTTGTGTGGCATTTCCCTCCATTG 228
DB 457 CAGGACACTGGCCATTGATATCCGACGTACATGAGATACCCCGGTGCAACC-----AT 404
QY 229 GATTAGTCGGGCGAAGTCACTCGGTATTTAATCCATCACTAAGAAATGTCACAGA 288
DB 403 TAGAATTTGGTCTTAACACCATCGGCATTTGAATTCGTCCCAAGAGAAATGTCAGA 344
QY 289 AATCTAAGTTTGTGAACCTGTGTCAGGCGTACTCGGGTAGGGTGTGTTGGTGGTTG 348
DB 343 AATCAAGATTGTTGAACCTGTGTTCAAGCGTACTCGGCCAATGTTGGTGGGTGACCAT 284
QY 349 ACCCGGTGCTGACGACACCAACCAATCAGTCATGACGAACTCTACCAAGCAC 408
DB 283 AGTTTGGCATGTAGGAGACCGTTTGAATCAGCGGTCTGACACTCGCTCGCCAGAAC 224
QY 409 CACCGAAGTTACATCCAGTACGCCCATATACGTGCCATCGTAGTCCCTAGGCCCAT 468
DB 223 CATCAAGTTGCAATTTGTTTCGGGGCCATATACGGGTCTCTGCTGTGCCAGCTGCG 164
QY 469 CAATGACCCCATTTGGCTCGATCGAGAGCTCGGGCACCGCCTATCGGGTCGATCGCG 528
DB 163 TTAAGACCAAGTTTGGCTTGAAGTTGTTGGCGCGCCACC--AGGCACCGCACCGAC 106

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QY 529 CCAACGATGTATGACAGTTGTT 552
 Db 105 CCAACGATGTATGACAGTTGTT 82

RESULT 9
 US-08-181-271A-4/c
 ; Sequence 4, Application US/08181271A
 ; Patent No. 5614395

GENERAL INFORMATION:
 ; APPLICANT: Ryals, John A.
 ; APPLICANT: Alexander, Danny C.
 ; APPLICANT: Beck, James J.
 ; APPLICANT: Duesing, John H.
 ; APPLICANT: Friedrich, Leslie B.
 ; APPLICANT: Goodman, Robert M.
 ; APPLICANT: Harms, Christian
 ; APPLICANT: Meins, Jr., Frederick
 ; APPLICANT: Montoya, Alice
 ; APPLICANT: Moyer, Mary B.
 ; APPLICANT: Neuhaus, Jean-Marc
 ; APPLICANT: Payne, George B.
 ; APPLICANT: Sperison, Christoph
 ; APPLICANT: Stinson, Jeffrey R.
 ; APPLICANT: Uknes, Scott J.
 ; APPLICANT: Ward, Eric R.
 ; APPLICANT: Williams, Shericca C.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 ; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CIBA-GEIGY Corporation
 ; STREET: 7 Skyline Drive
 ; CITY: Hawthorne
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10532

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/181,271A
 ; FILING DATE: 13-JAN-94
 ; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/093,301
 ; FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/937,197
 ; FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/678,378
 ; FILING DATE: 1-APR-1991

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/305,566
 ; FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/165,667
 ; FILING DATE: 8-MAR-1988

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/042,847
 ; FILING DATE: 6-APR-1993

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/632,441
 ; FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/425,504
 ; FILING DATE: 20-OCT-1989

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/848,506

FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/168,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/PL/CSC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 900 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 US-08-181-271A-4

Query Match 9.1%; Score 144.8; DB 1; Length 900;
 Best Local Similarity 60.5%; Pred. No. 6.2e-27;
 Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;

QY 45 GGTATCTTTGTTGAAAATTTGAAAGAAAGCTAGGACCAT-----GGACCTTGGG 99
 Db 607 GGCATCTTTCTTAAATAATCTGCACAAATCATGATAGGCCCATCATCCAGGCCCATTTG 548
 QY 100 TGCACAAATATTGTTGCTCCTCCAAATGTGGTACAAAGGATTTTACATCTCCGGGTACTT 159
 Db 547 TACACAAATATTCAITGGTITTTATCAGAGTACATGGGTTGTTACATCCACCTTGTGTTT 488
 QY 160 TAAGCTGACTAGACATTCACCATTTATTTTGGCGTGCATGAATGTGTGGCATTTCC 219
 Db 487 TCAACTGTGCTGGGCATTTGCTGTTAATAGGTGCTGTGCATCTGAGATTACGACAT---- 432
 QY 220 CTCCACTTGGATTAGTCGGGGGCGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAA 279
 Db 431 -----CTCCATTGGTCCGGCTGAATTCATGGGATGTTAATCCATCAACAGAGAGA 377
 QY 280 TGTCCAGAAATCTAAGTTGTTTAACTGGTCCAAAGCGTACTCGGCTAGGGTGTGTTGGTG 339
 Db 376 TGTGACAAAGTC---CTGATTGGGTTGATTAAAGTCAAAATTCAGTAAAGTGTAGGTG 320
 QY 340 GTTTGCCCCCAGCGGTGCTGCAGACACACCAATCACCAGTCATCGACGACCTC 399
 Db 319 CTTTCCATAGCCTTGACACTCTTACATCCCGTTACAGTCTCCAGTCTCACAATTACCTC 260
 QY 400 TACGACACACCGAAGTTTACATCCAGTACGACCCCATATAGTGCATCGTAGTGCCTC 459
 Db 259 GGCCACTGCCATCGAAGTTGCAATTTGGTTTCGACCCCAATTCGAGGCTGGAGCTGTTCTG 200
 QY 460 TAGGCGCATCAATGACCCACATTTGGCTCGATCGAGAGCTGGGACCGCCTATCGGT 519
 Db 199 GGTTCAATTAATGCTCCAAAGATTGGCTGAGTCGAGCGCCTGCTCCACC--TGGAGA 142
 QY 520 CGATGCCGCCCAACCGATGTATGACAGTTGTTGGCGGTACCTCGATATAGCAGCATAA 579
 Db 141 GGCCGGCGCCGACAGCTGTGTAGTGCATTTGTTGAC--NATGTCAAAAGTGCAGCATGA 84
 QY 580 GTGAAAGTCACAAA 593

Db 83 GTACAGCTACAAA 70
RESULT 10
US-08-449-315-4/c
; Sequence 4, Application US/08449315
; Patent No. 5650505
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,315
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506

; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-449-315-4
Query Match 9.1%; Score 144.8; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 6.2e-27;
Matches 335; Conservative 0; Mismatches 157; Indels 22; Gaps 5;
QY 46 GGTATCTTTTGGAAAAATGGAAAAAGACGTAGGACACAT-----GGACCTTGGG 99
DB 607 GGCATCTTTTCCTTAAAAAATCTCGACAAATCAGTAGGCCACATGATCCAGGCCCATTTG 548
QY 100 TGCACATATATTGTCTCCTCAATGTGGTACAGGATTGTGTACATCTCCGGGTACTT 159
DB 547 TACACATATATTCAATGGTTTATACAGTACATGGTTGTGTACATCCACTTGTGTTT 488
QY 160 TAAGCTGACTAGGACATTCACATTTATTTTCGGTGCATTTGAATTTGTGTGGCATTTCC 219
DB 487 TCAACTGTGCTGGGCATTTTCGTTAATAGTGTCTGTGCATCTGAGATTACGACAT---- 432
QY 220 CTCCACTTGGATTAGTCGGGCGAAAGTCATCGGTATATTAAATCCATCACTAAAGAAA 279
DB 431 -----CTCCATTTGGTGGGCTGAATTCATGGGGATGTTAAATCCATCAAGAGAGA 377
QY 280 TGTCCAGAAATCTAAGTTGTGAACTGGTCCAGGCGTACTCGGCTAGGGTGTTCGGTG 339
DB 376 TGTGCACAAAGTC---CTGATTGGTTGATTAAAGTCAAAATTCAGCTAAAGTTAGGTG 320
QY 340 GTTTGCCCCACCCGGTGCATCTGAGGACACCAACATCACCATCATGACGATCATGACGAACTC 399
DB 319 CTTTTCATAGCCTTGACACTCTAACATCCCGTTACAGTCTCCAGTCTCAATTAACCTC 260
QY 400 TACCAGCACACACCGAAGTTACATCCAGTAGGACCCCATATATACGTGCCATCGTAGTGCCC 459
DB 259 GGCCACTGCCATCGAAGTTGCAATTTGTTCCGACCCCAATGCCAGCTCGACTGTTCTTG 200
QY 460 TAGGGGATCAATGACCCCAATTTGGCTCGATGAGACCTCGGGGACCCGCTATCGGGT 519
DB 199 GGTTCAATTAATGCTCCAAAGATTGGCTGAGTCGAGCGCCCTCCCTCCACC--TGAGA 142
QY 520 CGATGCCGCCCAACACGATGTATGGACAGTTGTGGCGGTACCTCGATGTAGTACAGATAA 579
DB 141 GGCCGCCGCCGACACTGTGTAGGTGCAATTTGTTGAC--AATGTCAAAAGTGGCAGATGA 84
QY 580 GTGAAAGTCAAAA 593

83 GTAAACAGCTACAAA 70

Ov 580 GTGAAAGTCACAAA 593

Db 83 GTAACAGCTACAAA 70
RESULT 12
US-08-449-043-4/C
; Sequence 4, Application US/08449043
; Patent No. 5689044
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USSES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESS: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,043
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506

; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-449-043-4
Query Match 9.1%; Score 144.8; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 6.2e-27;
Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;
QY 46 GGTATCTTTTGTGAAAAAATGGAAAAAGACGTAGGACCACAT-----GGACCTTTGGG 99
Db 607 GGCATCTTTTCTTAAAAAATCTCGACAAATCAGTAGGCCACATGATCCAGGCCCAATTG 548
QY 100 TGCAACAATATGTTCCTCAAAATGGTACAGGATGTTTACATCCTCCGGGTACTT 159
Db 547 TACACAATATTCATTTGTTTATCACAGTACATGGGTTGTTTACATCCACCTTGTGTTT 488
QY 160 TAAGCTGACTAGGACATTCACCATTTATTTGCGGTGCATTTGAATTTGTGGCATTTCC 219
Db 487 TCACTGTGCTGGGCATTTGTCGTTAATAGTGTCTGTCATCTGAGATTACGACAT---- 432
QY 220 CTCCACTTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAATTCATCAACTAAAGAAA 279
Db 431 -----CCTCCATTTGTCGGGCTGAATTCATGGGGATGTTAAATCCATCAACAAGAGA 377
QY 280 TGTCCACAGAAATCTAAGTTGTTGAACCTGGTCCAGGGGTACTCGGCTAGGTTGTTGGTG 339
Db 376 TGTGACAAAGTC---CTGATGGGTTGATTAAGTGAATTCAGCTTAAGTGTAGGTG 320
QY 340 GTTTGCCCCCACCCTGGTGCATTCAGGACACCAACAATCAACAGTCAATGCACCAACCTC 399
Db 319 CTTTTCATAGCCTTGACACTTAACATCCCGTTACAGTCTCCAGTCTCACAATTAACCTC 260
QY 400 TACCAGACACCGAAGTTACATCCAGTACAGCCCATATACGTGCCATCGTAGTGCCC 459
Db 259 GGCCACTGCTCAAGTTGCAATTTGGTTCACCCCAATGCGAGCTGGACTGTTCTGT 200
QY 460 TAGCGCATCAATGACCCACACATTTGGCCTCCATCGAGACGTTCGGGCGACCGCTATCGGGT 519
Db 199 GGTTCACATTAATGCTCCAGATTGGCTGAGTCGAGCCGCTGCCCTCCACC--TGGAGA 142
QY 520 CGATGCCGCCCAAGAGATGATGACAGATGTTGTTGGCGGTACCTCGATGACAGCAATAA 579
Db 141 GGCCGCGGCCAGACTGTGTAGTGCATTTTGTGTAC--AATGTCAAAAGTGGCAGCATGA 84
QY 580 GTGAAAGTCACAAA 593

Db 83 GTAAACAGCTACAAA 70

RESULT 13

US-08-456-265A-4/c
; Sequence 4, Application US/08456265A
; Patent No. 5767369
; GENERAL INFORMATION:
; APPLICANT: Alexander, Danny C.
; APPLICANT: Ryals, John A.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Stinson, Jeffrey R.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,265A
; FILING DATE: 31-MAY-95

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/181,271
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018

; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19825/Pl/CGC 1727/DIV10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-456-265A-4

Query Match 9.1%; Score 144.8; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 6.2e-27;
Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;

QY	46	GGTATCTTTTGTGAAAAATTGGAAGAAAGCTAGGACACAT-----GGACCTTGGG	99
Db	607	GGCATCTTTTCTTAAAAAATCTCGAATAATCAGTAGGCCACATGATCCAGGCCCATTTG	548
QY	100	TGCAACAATATTGTTGCTCTCCAAATGTGGTACAAAGATTGTACATCTCCGGGTACTT	159
Db	547	TACACAATATTCAATGGTGTATTCACAGTACATGGTGTGTACATCCACCTTGTGTTT	488
QY	160	TAAGCTGACTAGGACATTCACCATTTATATTTTGGCCGTGCAATGAATGTGTGGCATTTCC	219
Db	487	TCAACTGTGTGGGCATTGTTCTTAATAGGTGCTGTGCATCTGAGATTACGACAT----	432
QY	220	CTCCACTTGGATTAGTCCGGGGGAAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAA	279
Db	431	-----CTTCATTTGGTGGGCTGAATTCATGGGGATGTTAAATCCATCAACAGAGAGA	377
QY	280	TGTCCCGAATACTAAGTTGTTGAACTGGTCCAAGCGCTACTCGGTAGGGGTGTTTGGTG	339
Db	376	TGTCGACAAAGTC--CTGATTGGGTTGATTAAATGCAAAATTCAGCTAAAGTGTAGGTG	320
QY	340	GTTTGGCCACCGGTGCACTGCAGACACACCACCAATCACCAGTCATGCAGAACCTC	399
Db	319	CTTTTCCATAGCCTTCACACTCTTAACATCCCGTTACAGTCTCCAGTCTCACAAATTACCTC	260
QY	400	TACCAGCACACCGAAAGTTACATCCAGTACGACCCCATATAGTGCCATCGTAGTCCCCC	459
Db	259	GGCACTGCGCATCGAAGTTGCAATTGGTTGACCCCAATCGAGGCTGGACTGTTCTTG	200
QY	460	TAGCGCATCAATGACCCACATTTGGCCTCGATCGAGAGCTGGGCAACCGCCTATCGGGT	519
Db	199	GGTTCACTAATGCTCCAAAGATTGGCCTGAGTCGAGCGCGCTGCCCTCCACC--TGAGAG	142
QY	520	CGATGCCGCCCAACGATGTATGACAGTTGTTGGCGGTACCTCGATAGTGACAGCATAA	579
Db	141	GGCCGGGCCACAGCTGTAGTGCAATTTGTTGAC--ATGTCAAAAGTGGCAGCATGA	84
QY	580	GTGAAAAGTCACAAA	593
Db	83	GTAACAGCTACAAA	70

RESULT 14

US-08-455-416-4/c
; Sequence 4, Application US/08455416
; Patent No. 577200
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.

APPLICANT: Duesing, John H.
 APPLICANT: Friedrich, Leslie B.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Harms, Christian
 APPLICANT: Meins, Jr., Frederick
 APPLICANT: Montoya, Alice
 APPLICANT: Moyer, Mary B.
 APPLICANT: Neuhaus, Jean-Marc
 APPLICANT: Payne, George B.
 APPLICANT: Sperison, Christopher
 APPLICANT: Stinson, Jeffrey R.
 APPLICANT: Uknes, Scott J.
 APPLICANT: Ward, Eric R.
 APPLICANT: Williams, Shericca C.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/08/455,416
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/181,271
 FILING DATE: 13-JAN-94
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
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 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 900 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-455-416-4
 Query Match 9.1%; Score 144.8; DB 1; Length 900;
 Best Local Similarity 60.5%; Pred. No. 6.2e-27;
 Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;
 QY 46 GGTATCTTTTGTGAAAAAATTTGAAAAAGACGTAGGACACACAT-----GGACCTTGGG 99
 Db 607 GCATCTTTTCTTAAAAAATCTCGACAAATCAGTAGGCCACATCATCCAGGCCCATTTG 548
 QY 100 TCGAACAAATATTGTTGCTCCTCAAATGGTACAAAGATTGTTACATCTCTCGGGTACTT 159
 Db 547 TACAAACAATATTGTTGTTTATTCACAGTACATGGGTTGTTACATCCACCTTGTGTT 488
 QY 160 TAAGCTGACTAGGACATTCACATTTATTTGCGTGCATTGATTTGTTGGCATTTCC 219
 Db 487 TCAACTGTGCTGGGCATTTGTTGTTTATAGTGTGTCATCTGAGATTACGACAT---- 432
 QY 220 CTCACATTTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCAATAAGAAA 279
 Db 431 -----CCTCCATTTGGTCGGGCTGAATTCATGGGGATGTTAAATCCATCAACAAGAGA 377
 QY 280 TGTCCACAGAAATCTAAGTTGTTGAACCTGCTCAAGGCGTACTCGGTAGGGTGTGGTG 339
 Db 376 TGTGACAAAGTC---CTGATTGGGTTGATTAAAGTGCAAATTCAGCTAAAGTGTAGGTG 320
 QY 340 GTTTGCCCCACCCGGTGCATCTGCAGGACACACCAATCAACAGTCATGACGAACTC 399
 Db 319 CTTTTCATAGCCTTGACACTTAACATCCCGTTACAGTCTCCAGTCTCACAATTACCTC 260
 QY 400 TACGAGCACACCGAAGTTACATCGAGTACAGCCCATATAGTGGCCATCGTAGTGGCCCC 459
 Db 259 GGCACCTGCCATCGAAGTTGCAATTTGGTTGACCCCAATCGAGCGCTGGACTTTCTGTG 200
 QY 460 TAGGCGCATCAATGACCCACATTTGGCTCGATCGAGACGTCGGGCGACCGCTATCGGT 519
 Db 199 GGTTCACATTAATGCTCCAAGATTGGCTGAGTCGAGCGGCTGCCTCCACC--TGGAGA 142
 QY 520 CGATGCCGCCCAACAGATGTATGGACAGTTTGGCGGTACTCTGATAGTGACAGCAATAA 579
 Db 141 GCGCGCGGCCAGACTGTGTAGTGCATTTTGTGTGAC--AATGTCAAAAGTGGCAGCATGA 84
 QY 580 GTGAAAGTCACAAA 593
 Db 83 GTACAGCTACAAA 70

RESULT 15
 US-08-455-244-4/c
 ; Sequence 4, Application US/08455244
 ; Patent No. 5789214
 ; GENERAL INFORMATION:
 ; APPLICANT: Ryals, John A.
 ; APPLICANT: Alexander, Danny C.
 ; APPLICANT: Beck, James J.

APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Melms, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19895/Pl/CSC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-455-244-4

Query Match 9.1%; Score 144.8; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 6.2e-27;
Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;

Qy	46	GGTATCTTTGTTGAAATAATGGAAAGACGTAGGACACAT-----GGACCTTGGG	99
Db	607	GGCACTTTTCTTAAATAATCTGCACAAATCAGTAGGCCCAATGATCCAGGCCCATTTG	548
Qy	100	TGCAACAATATTGTTGTCCTCCAAATGTTGTTACAAAGGATTGTATCATCTCCGGGTACTT	159
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Qy	160	TAAGCTGACTAGGACATTCACCATTTATATTGTCGTGCATTAATGTTGTCGATTTCC	219
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Qy	280	TGTCACGAAATCTAAGTTGTTGAACTGTCAGAGCGTACTCGGCTAGGTGTTTGGTG	339
Db	376	TGTCGACAAAGTC---CTGATTGGGTTGATTAAAGTSCAAATTCAGCTAAAGTTTAGGTG	320
Qy	340	GTTCGCCCAACCGGTGCCTGCAGGACACCAACCAATCACCAGTCATGCACGAACTTC	399
Db	319	CTTTTCATAGCCTTCACACTCTAACTCCGTTACAGTCTCCAGTCTCACAATTACCTC	260
Qy	400	TACCAGCACACGAAAGTTACATCCAGTACGACCCCATATAGTGCATCGTAGTCCCC	459
Db	259	GGCCACTGCCATCGAAAGTTGCAATTGGTTCCGACCCCAAAATGCGAGCTGGACTGTCTG	200
Qy	460	TAGGCGCATCATGACCCCATTTGGCCTCGATCGAGAGCTGGGCGACCGCCTATCGGGT	519
Db	199	GGTTCACATTAAATGCTCCAGATTGGCCTGAGTGGCGCGCTGCTCCACC--TGAGA	142
Qy	520	CGATGCCGCCCAACGATGTATGGACAGTTGTTGGCGGTACTTCGATAGTAGACAGATAA	579
Db	141	GGCCGCGGCCACGACTGTGTAGTGCATTTGTTGAC--AATGTCAAAGTGGCAGCATGA	84
Qy	580	GTGAAAGTACAAA	593
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Job time : 126.079 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 07:30:51 ; Search time 702.729 Seconds
(without alignments)
11157.588 Million cell updates/sec

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Perfect score: 1598
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
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- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
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- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1334.4	83.5	1546	14	US-10-051-307-3
4	291.2	18.2	510	16	US-10-341-961A-371
5	186.8	11.7	735	9	US-09-938-842A-2118
6	186.8	11.7	735	11	US-09-938-842A-2118
7	186.8	11.7	950	9	US-09-770-445-334
8	168.8	10.6	875	12	US-10-636-396-4
9	168.8	10.6	875	17	US-10-636-026-4
10	161.2	10.1	909	13	US-10-424-599-103619
11	158.4	9.9	1956	13	US-10-424-599-36321
12	137.2	8.6	1173	13	US-10-424-599-7736
13	136.8	8.6	717	15	US-10-259-165-389
14	136.8	8.6	720	15	US-10-259-165-41

C 15	134.6	8.4	1006	17	US-10-437-963-86607
C 16	129	8.1	901	13	US-10-424-599-7737
C 17	119.4	7.5	911	13	US-10-425-114-27634
C 18	118.6	7.4	696	15	US-10-259-165-353
C 19	118.6	7.4	699	15	US-10-259-165-109
C 20	118.6	7.4	1052	17	US-10-437-963-89569
C 21	115.8	7.2	1020	15	US-10-259-165-371
C 22	115.8	7.2	1020	16	US-10-260-238-3136
C 23	113.2	7.1	879	16	US-10-260-238-49
C 24	109.4	6.8	805	16	US-10-260-238-4061
C 25	108.2	6.8	922	16	US-10-260-238-4067
C 26	105.6	6.6	808	9	US-09-966-881-46
C 27	101.6	6.4	633	15	US-10-259-165-532
C 28	101.6	6.4	633	16	US-10-260-238-5182
C 29	99.8	6.2	3630	17	US-10-437-963-16245
C 30	97	6.1	1950	17	US-10-437-963-59877
C 31	94.2	5.9	343	9	US-09-770-791-806
C 32	90.8	5.7	869	17	US-10-437-963-15621
C 33	90.6	5.7	621	15	US-10-175-389-9
C 34	89.2	5.6	621	15	US-10-175-389-1
C 35	85.6	5.4	728	16	US-10-260-238-3135
C 36	84.6	5.3	1928	13	US-10-425-114-24457
C 37	75.8	4.7	695	15	US-10-259-165-630
C 38	75.2	4.7	973	17	US-10-437-963-16928
C 39	74.4	4.7	826	13	US-10-425-114-23076
C 40	73.2	4.6	730	13	US-10-425-114-25389
C 41	70.2	4.4	935	17	US-10-437-963-82256
C 42	69.4	4.3	777	15	US-10-259-165-229
C 43	68.8	4.3	529	14	US-10-051-307-6
C 44	67.8	4.2	891	17	US-10-437-963-49328
C 45	66.4	4.2	904	13	US-10-425-114-28239

ALIGNMENTS

RESULT 1

US-10-051-307-2
; Sequence 2, Application US/10051307
; Publication No. US20020170095A1
; GENERAL INFORMATION:
; APPLICANT: DALI, ZIYU
; APPLICANT: SHI, LIFANG
; APPLICANT: HOOKER, BRIAN S.
; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
; FILE REFERENCE: 059440/0141
; CURRENT APPLICATION NUMBER: US/10/051,307
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,224
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1598
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-051-307-2

Query Match	100.0%	Score	1598	DB	14	Length	1598
Best Local Similarity	100.0%	Pred. No	0				
Matches	1598	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	GTAATAGACTCACTATAGGGCACGGTGTGACGCCCGGGTGGTATCTTTGTTGA	60				
Db	1	GTAATAGACTCACTATAGGGCACGGTGTGACGCCCGGGTGGTATCTTTGTTGA	60				
QY	61	AAAAATTGGAAGAAAGTAGGACCATGACCTGGTGCACAAATATTGTTGCTC	120				
Db	61	AAAAATTGGAAGAAAGTAGGACCATGACCTGGTGCACAAATATTGTTGCTC	120				
QY	121	CAATGTGGTACAAGGATTGTTACATCTCCGGGTACTTTAAGCTGACTAGGACATTAC	180				
Db	121	CAATGTGGTACAAGGATTGTTACATCTCCGGGTACTTTAAGCTGACTAGGACATTAC	180				

D _b	301	TGAAC TTGTTCC AAGCGTACT CGGTAGGGTGTTTGGTGGTTTGCCCAACCGGTGCAC T	360
Q _y	361	GCAGGACACCACA CAATCACCAGTCATGCAGAACTCTACGAGCACCCGAAGTTAC	420
D _b	361	GCAGGACACCACA CAATCACCAGTCATGCAGAACTCTACGAGCACCCGAAGTTAC	420
Q _y	421	ATCCAGTAGCAGCCCATATACGTCGCCATCGTAGTGCCCTAGGCGCATCAATGACCCACA	480
D _b	421	ATCCAGTAGCAGCCCATATACGTCGCCATCGTAGTGCCCTAGGCGCATCAATGACCCACA	480
Q _y	481	TTTTGGCCTCGATCGAGACGCTCGGCGCACCGCTATCGGGTCGATGCGGCCAAAACGATGTA	540
D _b	481	TTTTGGCCCCGATCGAAAACGTCGCCACCCGCTTTGGGGTCGATGCGGCCAAAACGATGTA	540
Q _y	541	TGACACAGTTGTTGGCGGTACTCGATAGTAGCAGCATATAGTGNAAAGTCACRAAAGCCAGA	600
D _b	541	TGGACACAGTTGTTG - CGTAGCTCGATAGTGGCAGCATATAGTGNAAAGTCACRAAAGCCAGA	598
Q _y	601	AGGGAGAAAACAAAAGAAAGATCTCAAGTAGGCCCATCGTTTGGTTGAAATTTATATGTGGACA	660
D _b	599	AGGGAGAAAACAAAAGNAGATCTCAAGTAGGCCCATCGTTTGGTTGAAATTTATATGTGGACA	658
Q _y	661	AATTATTTTTGGTACTTTTATATATAGGGATATGCGCGCTTTTGGGACACTACGATATTATAT	720
D _b	659	AATTATTTTTGGTACTTTTATATATAGGGATATGCGCGCTTTTGGGACACTACGATATTATAT	718
Q _y	721	CGTATTATATAACAATATCATCTTTGACTAAATTATAAACGAAATATATTACAATATGAT	780
D _b	719	CGTATTATATAGCANATATCATCTTTGACTAAANTATTAACGAAATATATTACAATATGAT	778
Q _y	781	TTGGTAAACCGTTGAGGTGGAAAAATGTATAGAGCGCCCTAATAATAATTATTTATATGA	840
D _b	779	TTGGTAAACCGTTGAGGTGGAAAAATGTATAGAGCGCCCTAATAATAATTATTTATATGA	838
Q _y	841	ATATAGCCTATAGTTACAAGTTAACTTTATTTGGTGATAACTTTTGACATATAAATCTCTGT	900
D _b	839	ATATAGCCTATAGTTACAAGTTAACTTTATTTGGTGATAACTTTTGACATATAAATCTCTGT	898
Q _y	901	AACGTGACGGAAATTTTTCTTAAAACCTAAATATTAAAAAGCAGCTATTTTCACATTTTTTCG	960
D _b	899	AACGTGACGGAAATTTTTCTTAAAACCTAAATATTAAAAAGCAGCTATTTTCAGATTTTTTCG	958
Q _y	961	TGGCCAAAGTCCTGTGCATACCTATATATGCGCATTTTTTTACTTTTATCGTTCTAGGCTTC	1020
D _b	959	TGGCCAAAGTTCTTGCATACCTATATCTATGCCCCATTTTTTACTTTTATCGTTCTAGGCTTC	1018
Q _y	1021	TAGGTACACGTTTCGAACATAAAAATCATAAAAATTCGAAAGTAAAAATAGTTTTTTTTTT	1080
D _b	1019	TAGGTACACGTTTGAACATAAAAATCATAAAAATTCGAAAGTAAAAATAGTTTTTTTTTT	1078
Q _y	1081	TTTCATATTACTCGTATGTCATTTGTTAGATCAATCTGAAATATACAAACCATTCTGAT	1140
D _b	1079	TTTCATATTACTCGTAGGGATCATTTGTTTAGATCAATCTGAAATATACAAACCATTCTGAT	1138
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D _b	1139	TTTAAATACAAACCATTTCTGCC--AAGGGGAAGCTCTATGATCCCGTGCAAGTGTTTT	1196
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D _b	1257	CCTATTGTATGCAAAATATCTATTAAAGAACCCCTATTTCATCTTTTATTTTATTTTACGAT	1316
Q _y	1320	CGGAGCATGGATATATTTTACTAAATTTAAATATAAATTTGGGAGGAATGTATCGACAAGCCATC	1379
D _b	1317	CGGAGCATGGATATATTTACTAAATTTAAATATAAATTTGNAAGGAATGTATCGACAAGTCATC	1376
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Qy	1440	GGATCATGTACAAATTCGAGTTTAAAAAATATCTCCTATATAAATACCTGTCTATCTCCCTCTTAAA	1498
Db	1437	GGATCATGTATTAATTTAGTTTAAATATCTCCTATAAATATCTATATATACCTCTAAA	1496
Qy	1500	CCAAATACATCTTAAACACACAAAATATAAACTTAGATTCCTTAAGCAAAATTCGCAAAATAA	1559
Db	1497	CTAAATGCATCTTAAACACACAAAATATAAACTTAGATTCCTTTAAGAAATTTGCAAAATAA	1556
Qy	1560	ATGGAGGCAAAATAGTCTATGGTGAAGTTGGTTGCTTTC	1598
Db	1557	ATGGAGGCAAAATAGTCTATGGTGAAGTTGGTTGCTTTC	1595

RESULT 3

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US-10-051-307-3
; Sequence 3, Application US/10051307
; Publication NO. US20020170095A1
; GENERAL INFORMATION:
; APPLICANT: DAI, ZIYU
; APPLICANT: SHI, LIFANG
; APPLICANT: HOOKER, BRIAN S.
; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
; FILE REFERENCE: US9440/0141
; CURRENT APPLICATION NUMBER: US/10/051,307
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,224
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1546
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1248)
; OTHER INFORMATION: a, t, c or g
US-10-051-307-3

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Query Match 83.5%; Score 1334.4; DB 14; Length 1546;
Best Local Similarity 93.8%; Pred. No. 7.1e-286;
Matches 1456; Conservative 0; Mismatches 87; Indels 10; Gaps 6

QY	49	ATCTTTGTTTGA	AAAATTGG	GA	AAAGAC	GTG	AGACCA	CTG	AGACCT	TGG	TGGT	GGCA	CAAT	108
DB	1	ATCTTTGTTTGA	AAAAATTG	GA	AAAGAA	ACG	TAGGAC	CCATG	AGACCT	TGG	TGGT	GGCA	CAAT	60
QY	109	ATTGTTGCC	CCAAATG	TG	CTACA	AGG	ATTGTT	TAC	ATCTCC	CGG	GTATCTT	TAAGCT	GCAC	168
DB	61	ATTGTTGCC	CCAAATG	TG	CTACA	AGG	ATTGTT	TAC	ATCTCC	CGG	GTATCTT	TAAGCT	GCAC	120
QY	169	TAGGAC	ATTCA	CCATT	TATAT	TTT	GCCG	TGCA	TTG	GAATT	GTG	TGG	GCAATT	228
DB	121	TAGGAC	ATTCA	CCATT	TATAT	TTT	GCCG	TGCA	TTG	GAATT	GTG	TGG	GCAATT	180
QY	229	GATTAG	TCGGGG	CG	GAAG	CTCAT	CGGTAT	ATT	AAATCC	ATCACT	AAAGAA	TGTC	CCGAGA	288
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QY	289	AATCT	TAAGTTG	T	TGA	ACT	TGGT	CC	AAAGGG	CTACT	CGGCT	TAGG	TGTTT	348
DB	241	AATCT	TAAGTTG	T	TGA	ACT	TGGT	CC	AAAGGG	CTACT	CGGCT	TAGG	TGTTT	300
QY	349	ACCCGGT	GCATC	G	CAGG	ACAC	CA	CAAT	CA	CCAGT	CA	TGCA	CAGAA	408
DB	301	ACCCGGT	GCATC	G	CAGG	ACAC	CA	CAAT	CA	CCAGT	CA	TGCA	CAGAA	360
QY	409	GACCGA	GTTAC	AT	CCAGT	ACG	ACCC	CA	TATAC	GTG	CCCAT	CGT	TAGT	468
DB	361	CATCGA	AGTTAC	AT	CCAGT	ACG	ACCC	CA	TATAC	GTG	CCCAT	CGT	TAGT	420
QY	469	CAATG	ACCC	CA	ATT	T	TGG	CTC	AT	CGAG	ACG	TCGGG	CA	527

US-09-938-842A-2118/c
; Sequence 2118, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SRIPI300-3
; CURRENT FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2118
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2118

Query Match 11.7%; Score 186.8; DB 9; Length 735;
Best Local Similarity 62.4%; Pred. No. 3.1e-31;
Matches 367; Conservative 0; Mismatches 202; Indels 19; Gaps 4;

Qy 46 GGATCTCTTTGTTGAAAATAATGGAAGAACGCTAGGACACATG-----GACCTTGGG 99
Db 586 GGCATCTCTGTTAAAGAAATCTTGAGTACTCAGTATCGGTACATGATCCCTGACCGGTG 527

Qy 100 TGCACATATGTTGCTCCAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 159
Db 526 TACAACAGTATGTTGCTGCTGAAATACAGTACACGGGTTGTTGATCCACCTCGGGCTC 467

Qy 160 TAAGCTGACTAGGACATTCACCATTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 219
Db 466 TCAACAGTTTGGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408

Qy 220 CTCACCTTGGATAGTCGGGCGAAGTATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 279
Db 407 -----GAACCTAGTTGGGCTAAACTCCATAGTATGTTAAATCCATCGACAAAGTAGA 356

Qy 280 TGTCCGAAATCTAAGTTGTTGAACTGCTCAAGGCGTACTCGGCTAGGCTGTTGGTG 339
Db 355 TATCGTAGAGTCTAAGTTGTTGAACTGCTCAAGGCGTACTCGGCTAGGCTGTTGGTG 296

Qy 340 GTTTCGCCACCCGGTGCACTGCGAGGACACCAACCAATCAACGATGATGACGAACTC 399
Db 295 GCTGTCCCGACGAGTACATTTGAGTCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 236

Qy 400 TACGAGCACCCGAGTACATTTGGCTCGATCGAGACGCTCGGCGACCGCTATCGGGT 459
Db 235 GACCTGAGAGTCAAAAGTTACAAATTTGCTTACCCCAATCCGTCGCTGCTGCTGCTGCTG 176

Qy 460 TAGGCGCATCAATGACCCACATTTGGCTCGATCGAGACGCTCGGCGACCGCTATCGGGT 519
Db 175 CCGGACATCTAGCTTCCATGATTTGGCGAGCATCTAGAGCTGCGGCCACTCC--AGGGCT 118

Qy 520 CGATCGCGCCCAACGATGATGAGCAGTTGTTGGCGTACTCTGATAGTACAGCAGATAA 579
Db 117 TCGCGCAGCCCAACGCTGTAATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60

Qy 580 GTGAAGTCAAAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAG 627
Db 59 GCGGTGGAGATGACGCAAAAGTCCGGAATATGAAAGTAGAGACCAAG 12

RESULT 6
US-09-938-842A-2118/c

; Sequence 2118, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SRIPI300-3
; CURRENT FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2118
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2118

Query Match 11.7%; Score 186.8; DB 11; Length 735;
Best Local Similarity 62.4%; Pred. No. 3.1e-31;
Matches 367; Conservative 202; Indels 19; Gaps 4;

Qy 46 GGATCTCTTTGTTGAAAATAATGGAAGAACGCTAGGACACATG-----GACCTTGGG 99
Db 586 GGCATCTCTGTTAAAGAAATCTTGAGTACTCAGTATCGGTACATGATCCCTGACCGGTG 527

Qy 100 TGCACATATGTTGCTCCAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 159
Db 526 TACAACAGTATGTTGCTGCTGAAATACAGTACACGGGTTGTTGATCCACCTCGGGCTC 467

Qy 160 TAAGCTGACTAGGACATTCACCATTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 219
Db 466 TCAACAGTTTGGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408

Qy 220 CTCACCTTGGATAGTCGGGCGAAGTATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 279
Db 407 -----GAACCTAGTTGGGCTAAACTCCATAGTATGTTAAATCCATCGACAAAGTAGA 356

Qy 280 TGTCCGAAATCTAAGTTGTTGAACTGCTCAAGGCGTACTCGGCTAGGCTGTTGGTG 339
Db 355 TATCGTAGAGTCTAAGTTGTTGAACTGCTCAAGGCGTACTCGGCTAGGCTGTTGGTG 296

Qy 340 GTTTCGCCACCCGGTGCACTGCGAGGACACCAACCAATCAACGATGATGACGAACTC 399
Db 295 GCTGTCCCGACGAGTACATTTGAGTCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 236

Qy 400 TACGAGCACCCGAGTACATTTGGCTCGATCGAGACGCTCGGCGACCGCTATCGGGT 459
Db 235 GACCTGAGAGTCAAAAGTTACAAATTTGCTTACCCCAATCCGTCGCTGCTGCTGCTGCTG 176

Qy 460 TAGGCGCATCAATGACCCACATTTGGCTCGATCGAGACGCTCGGCGACCGCTATCGGGT 519
Db 175 CCGGACATCTAGCTTCCATGATTTGGCGAGCATCTAGAGCTGCGGCCACTCC--AGGGCT 118

Qy 520 CGATCGCGCCCAACGATGATGAGCAGTTGTTGGCGTACTCTGATAGTACAGCAGATAA 579
Db 117 TCGCGCAGCCCAACGCTGTAATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60

Qy 580 GTGAAGTCAAAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAG 627
Db 59 GCGGTGGAGATGACGCAAAAGTCCGGAATATGAAAGTAGAGACCAAG 12

RESULT 7
US-09-770-445-334/c
; Sequence 334, Application US/09770445

```

; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Naja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hufban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PAPA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334
; LENGTH: 950
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-334

Query Match      11.7%; Score 186.8; DB 9; Length 950;
Best Local Similarity 62.4%; Pred. No. 3.6e-31;
Matches 367; Conservative 0; Mismatches 202; Indels 19; Gaps 4;

QY 46 GGTATCTCTTTGTTGAAAGAAATGGAAGAAACGTAGGACACATG-----GACCTTGGG 99
DB 594 GGCATCTCTGCTTAAGAAATCTTGAGTACTGCTACATGCTGCTACATGATCCCTGACCTTGC 535
QY 100 TGAACACATATGTTGCTCCAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 159
DB 534 TACAACAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 475
QY 160 TAAGCTGACTAGGACATTCACCAATTTATATTTCCCGTGCATTTGAATTTGTTGTTGTTGTT 219
DB 474 TCAACAGTTTGACATTTGCTCCGTTTATGTTGCTGCTGATATGATATCCGATGGAGTTTC 416
QY 220 CTCACCTGATTTAGTGGGGCGAAAGTCACTGGTATATTTAAATCCATCAACTAAAGAAA 279
DB 415 -----GAACTAGTTGGGCTAAACTCCATAGTATGTTAAATCCATCGACAAAGTGAGA 364
QY 280 TGTCCAGAAATCTAAGTTGTTGAACTGTGCTCAAGCGTACTCGCTAGGTTGTTGTTGTTG 339
DB 363 TATCGTAGAAGTCTAAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 304
QY 340 GTTTGCCCCACCGGTGCTACTGAGGACACCAACCAATCACCAGTCAATGCAACGAACCTC 399
DB 303 GCTGTCCCCAGCGAGTACATTTGGAGTCCACCACTGCAGTCCACAGTTTGGCATCGGCCAC 244
QY 400 TACCAGCACCCAGAGTTACATCCAGTACGACCCCATATAGTGGCATCTGTTAGTGGCCC 459
DB 243 GACCTGAGGAGTCAAAAGTTTACAAATGGTCTTACCCCAATCCGTTGCCAATTTTGTGGCC 184
QY 460 TAGGCGCATCAATGACCCACATTTGGCCCTCGATTCGAGACGTGCGGCACCGCCTATCGGGT 519
DB 183 CCGCGACATCTAGCTCCCATGATTTGGCCAGCATCTAGAGCTGGGCCACCTCC--AGGGCT 126
QY 520 CGATGCCGCCAAACGATGTATGGACAGTTGTTGGGGTACTCTGATAGTGACAGATAA 579

; Db 125 TCGCGCAGCCCAACACGGTGTAACTACATTTGTT--TAGGATTTCCGAATGTGCGGCTGTT 68
; QY 580 GTCAAAAGTCACAAAAGCCAGAAAGGAGAAACCCAAAGAAAGATCTCAAG 627
; Db 67 GCGGTGGAGATGAGCAAAAGTCCGGAATAATATGAANGTAGAGACCAAG 20

RESULT 8
US-10-636-396-4/c
; Sequence 4, Application US/10636396
; Publication No. US20040073971A1
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/10/636,396
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-10-636-396-4

Query Match      10.6%; Score 168.8; DB 12; Length 875;
Best Local Similarity 61.3%; Pred. No. 3.4e-27;
Matches 309; Conservative 0; Mismatches 167; Indels 8; Gaps 2;

QY 49 ATCTTTGTTGTTGAAAAAATGGAAGAAACGTAGGACACATGACCTTGGGTGCAACAAT 108
DB 577 ATCTGGTCTTTGAAAAAACCTTTGATAAATCAGTTGGTCCACAATTTCCAGAGTTGCAACAAT 518
QY 109 ATTGTGTCCTCCAAATGTGGTACAAGATTGTTTACATCTCCGGGTACTTTAAGCTGAC 168
DB 517 ACTGATCAGTTTGTACACGGTGCNAGGTTATTGACCCGCGAGGAGCCGTAATCTAC 458
QY 169 TAGACATTCACATTTATATTTGCCGTGCAATTAATGTTGGCATTTTCCCTCCACTTG 228
DB 457 CAGGACACTGCGCATTTGATATCCGCACTACATGAGATACCCCGGTGTCACCC-----AT 404
QY 229 GATTAGTCGGGGCGAAAGTCACTCGGTATATTAAATCAATCACTAAGAAATCTCCCGA 288
DB 403 TAGAATTTGGTCTTAACACCATCGGCATTTGAATTCGTCCCAAGAGAAATGTCAAAGA 344
QY 289 AATCTAAGTTTGTGAATCGTCCAGGCGTACTCGGTAGGGTGTGTTGTTGTTGTTGTTG 348
DB 343 AATCAAGATTGTTGAATCGTCCAGGCGTACTCGGCAATGTTGGGTGGGTGGGTACCAT 284
QY 349 ACCCGGTGCTACGAGACACCAACCAATCACCAGTCACTGACGACACCTTACAGGAC 408
DB 283 AGTTTGGCATTTGAGAGAGACCGTTGCAATCACCGGTCTGACACCTGCTCGCCGAGAAC 224
QY 409 CACGAGATTACATCCAGTACGACCCCATATACGTGCTAGTGCCTAGGCGCAT 468
DB 223 CATCAAGATTGCAATTTGTTCCGGGCCATATACGGGCTCTCTGCTGTCGACGAGTGCACGG 164
QY 469 CAATGACCCACATTTGGCTCTGATCGAGAGTGGGCGACCGGCTATCGGGTGTATCGCCG 528
DB 163 TTAAGACAGAGTTTGGCTGAGTTAAGTTGTTGGCGCCGCCACC--AGGCACCGCACGAC 106

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Qy 529 CCAAAACGATGTATGGACAGTTGTT 552
 Db 105 CCAAAACGGTGTATGGACAGTTGTT 82

RESULT 9

US-10-636-026-4/c
 ; Sequence 4, Application US/10636026
 ; Publication No. US20040111761A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Crasta, Oswald R.
 ; APPLICANT: Duwick, Jon
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guhua
 ; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
 ; TITLE OF INVENTION: Genes and their Uses
 ; FILE REFERENCE: 5718-90
 ; CURRENT APPLICATION NUMBER: US/10/636,026
 ; CURRENT FILING DATE: 2003-08-07
 ; PRIOR APPLICATION NUMBER: US/09/589,733C
 ; PRIOR FILING DATE: 2000-06-08
 ; PRIOR APPLICATION NUMBER: 60/140,646
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/162,904
 ; PRIOR FILING DATE: 1999-11-01
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 875
 ; TYPE: DNA
 ; ORGANISM: Helianthus annuus
 US-10-636-026-4

Query Match 10.6%; Score 168.8; DB 17; Length 875;
 Best Local Similarity 61.3%; Pred. No. 3.4e-27;
 Matches 309; Conservative 0; Mismatches 187; Indels 8; Gaps 2;
 Qy 49 ATCTTTGTTTCAAAAAATTGGAAGACGATGACACATGACCTTGGGTGCAACAAT 108
 Db 577 ATCTGGCTTGAAGAACCTTGATTAATCAGTTGGTCCACAAATTCAGAGTTGCAACAAT 518
 Qy 109 ATTGTGTCCTCCAAATGTGTACAGAGTTGTTTACATCTCCGGGTACTTTAAGCTGAC 169
 Db 517 ACTGATCAGTTTGTACACGGTGAAGGTTATTGACCCGCCAGGAGCCCGTAATCTCAC 458
 Qy 169 TAGGACATCCACATTATATTTCCGTCGATTTGATTTGTGGCATTTCCCTCCACTTG 228
 Db 457 CAGGACACTGGCCATTGATATCCGCGATACATGAGATACCCCGGTGACCC-----AT 404
 Qy 229 GATTAGTCGGGGCGAAAGTCTATCGGTATATTAAATCCATCAACTAAAGAAATGTCCAGA 288
 Db 403 TAGAATTGGTCTAAACACCATCGGCACATTGAATCCGTCCACAAGAGAAATGTCAAAGA 344
 Qy 289 AATCTAAGTTGTGAACCTGGTCCAAAGGCTACTCGGCTAGGGTGTGTTGGTGGTGGCCCC 348
 Db 343 AATCAAGATTGTGAACCTGGTTCAAAGGCTACTCGGCGCAATGTGTGGTGGGTGGTACAT 284
 Qy 349 ACCCGGTGCATGTCAGGACACACCACCAATCACCAGTCTATGACGAACTCTACGACGAC 408
 Db 283 AGTTTGGCAATTGGAGGAGACCGTTGCAATCACCGTCTGACACTGCTCGCCAGNAC 224
 Qy 409 CACCGAAGTTATCCAGTACGACCCCATATACGTGCGCATCGTAGTGGCCCTCAGGCGAT 468
 Db 223 CATCAAGTTGCAATTGGTTCCGGGCCATATACGGGCTCCTGCTGTGCCAGTGCAGCG 164
 Qy 469 CAAACCCACATTTGGCTCGATCGAGNCGTCGGGACCGCCCTATCGGTCGATGCGGC 528
 Db 163 TTAAGAGACAGGTTTGGCTGAGTTAAGTTGTGCGCCGCCACC--AGCACCGCACGACG 106
 Qy 529 CCAAAACGATGTATGGACAGTTGTT 552
 Db 105 CCAAAACGGTGTATGGACAGTTGTT 82

RESULT 10

US-10-424-599-103619/c
 ; Sequence 103619, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 103619
 ; LENGTH: 909
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_64586C.1
 US-10-424-599-103619

Query Match 10.1%; Score 161.2; DB 13; Length 909;
 Best Local Similarity 61.1%; Pred. No. 1.7e-25;
 Matches 314; Conservative 0; Mismatches 193; Indels 7; Gaps 3;
 Qy 46 GGTATCTTTGTTGAAAAAATTGGAAGACGATGACACATGACCTTGGGTGCAAC 105
 Db 631 GGCACCTTTGCTTGAAGAATCTGGAATAATAGTGGGCCACAGCTACCGAATTTGCAAC 572
 Qy 106 AATATTGTTGCTCTCCAAATGTGTACAAGGATTGTTACATCTCCGGTACTTTAAGCT 165
 Db 571 AGTACTGGTCGGTTTGAAGACAGTCCAAGGTTGTTGCAACCTCTTGGAGCTTTAGCT 512
 Qy 166 GACTAGGACATTCACCAATTTATTTGCGGTGCGTGAATTTGTTGGCATTTTCCCTCCAC 225
 Db 511 CACTAGGCGACTGTCGGTTAATGTCGCGCAGTGCA--GCTTATGCCACGTTGTCATCCAT 455
 Qy 226 TTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCACTAAAGAAATGTCCC 285
 Db 454 TCG---AGGTGGACTAAAGTCCAGGACAGTTTAAACCGTCGACGAGGAGATGTGA 398
 Qy 286 AGAAATCTAAGTTGTTGAACTGCTGCCAAGCGCTACTCGGCTAGGGTGTGTTGGTGTTC 345
 Db 397 AGAAGTCCAAATTTGTAACCCGTTTCAGGCCGTTATTCAGCCAGGTTGTTGGAGGCGCAC 338
 Qy 346 CCACCCCGGTGCTGCTGACGACACACCAACATCACCAGTCTATGACGACGACCTTACCAG 405
 Db 337 CGTAAGCTTTGCACTGACGAGGACACCCCGCGAGTCACCGGTCTGGCATCCACCGCGCCG 278
 Qy 406 CACCACCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTAGTGCCTTAGGGG 465
 Db 277 AACCGTGAAGTTGACCGCGTTTCGGGCCCAACCGGGGCCCTTTTCGTTCTTGCAAGCA 218
 Qy 466 CATCAATGACCCACATTTGGCTCGATCGAGAGCTCGGCGACCGCTTATCGGGTCTGATG 524
 Db 217 CGTCCACGACCATGATGCTGGCCCGGTTTAAATTGCACGCGCACCGCCCAACAGGACAGCG 158
 Qy 525 CCGCCCAAGCATGTATGGACAGTTGTTGGCGT 558
 Db 157 CAGCCCAAGCATGTATGTGCTCGGTTGTGAT 124

RESULT 11

US-10-424-599-36321/c
 ; Sequence 36321, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 36321
 ; LENGTH: 1956
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(1956)
 ; OTHER INFORMATION: unsure at all n locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MET3847_132800C.1
 ; US-10-424-599-36321

Query Match 9.9%; Score 158.4; DB 13; Length 1956;
 Best Local Similarity 61.0%; Pred. No. 1.1e-24;
 Matches 317; Conservative 0; Mismatches 186; Indels 17; Gaps 3;

 QY 45 TGGTATCTTTGTTGAAAAATTTGAAAAAGAACGTAGGACCACA-----TGGACCTTGG 98
 Db TGGACCTTATCTTTGAAAAATTTGAAAAAGAACGTAGGACCACA-----TGGACCTTGG 1279

 QY 99 GTGCAACAATATTGTGTCCTCCAAATGTGTACAAAGATTTGTACATCTCCCGGTACT 158
 Db GTGCAACAATATTGTGTCCTCCAAATGTGTACAAAGATTTGTACATCTCCCGGTACT 1278

 QY 159 TTAAGCTGACTAGACATTCACCAATTTATTTCCCGTGTCAATTAATTTGTGTCGCAATTC 218
 Db CTTAATGCGCCCGGCACTGCGCAATTTGATATTCAGCGCTGCAATTTTGTGACACCCA 1159

 QY 219 CCTCCACTTGGATTAGTCGGGGCAAAAGTCAATCGGTATTTAAATCCATCAACTAAAGAA 278
 Db CCG-----TTTAGAGGTGAAGTCCATCGAATTTGAACCGTCCACCAAGAG 1108

 QY 279 ATGTCCAGAAATCTAAGTTGTGAATGCTGTCGAAAGCGTACTCGGCTAGGGTGTGTTGGT 338
 Db ATGTCTGAGAAATCTGTTGCAAAATTTGTTCAACCGCAATTCGCAAGTGTGTTGGGA 1048

 QY 339 GGTGTTGCCCAACCGGTGCACTGAGCAGACACCACCAATCAGCAGTCAGCAACCT 398
 Db GGGACCCCGCCCTTGGCAATGAGCGCCCGGTGCACTGCGGTGCGGTGCGGCGCGG 988

 QY 399 CTACGACACCAACGAAATTTACATCCAGTACGACCCCATATAGTGCATCGTGTGCGCC 458
 Db CGGCGGCTGCCATCAAAAGTTGCAACCGGTGCGGCGCCCATATAGCGGCAATGCGCGT 928

 QY 459 CTAGGCGCATCAATGACCGCAATTTGCGCTCGATCGAGCTGCGGACCGGCTATCGGG 518
 Db GGGTTTACCGAGGTTCCACGTTTGCCACCGGTTCAGACGCGCGGCTCCACC--CGGAC 870

 QY 519 TCGATGCGCGCCCAACCAATGATGGAAGTGTGTCGCGGT 558
 Db TCGCGCGCGCCCAACCAATGATGGAAGTGTGTCGCGGT 830

RESULT 12
 US-10-424-599-7736/c
 ; Sequence 7736, Application US/10/424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 7736
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(1173)
 ; OTHER INFORMATION: unsure at all n locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MET3847_106998C.1
 ; US-10-424-599-7736

Query Match 8.6%; Score 137.2; DB 13; Length 1173;
 Best Local Similarity 58.7%; Pred. No. 4.2e-20;
 Matches 303; Conservative 0; Mismatches 193; Indels 20; Gaps 3;

 QY 49 ATCTTTGTTTGAATAATTTGAAAAAGAACGTAGGACCACA-----TGGACCTTGGGTGC 102
 Db ACCTCTCTCTTTGAAGAACTTTGGAATAATCAGTGGGACCGCAACCCGCGACGCGGTGTAC 605

 QY 103 AACAATATTGTTGTCCTCCAAATGTGTACAAAGATTTGTATCATCTCCGGGTACTTTAA 162
 Db AACAGTACTGAGTCTGATTTGAAAAACCGTGCACGGGTGTTGACGCGCGCGGAACTGAA 545

 QY 163 GCTGACTAGGACATTCACCAATTTATTTGCGTGCATTTGAATTTGTGTCGCAATTTCCCTC 222
 Db GCTGAGTGGACACTCTCGATGATGTCGCGCGCGCATTTCCAGGAGTGCAGTTG----- 489

 QY 223 CACTTGGATTTAGTCGGGCGGAAAGTCATCGGTATATTAAATCCATTCAACTAAAGAAATGT 282
 Db -----TAGTTCGGGCTCACCTGCAAGGGAATGTTGAAACCGTGCACGAGGAGATGT 437

 QY 283 CCCGAAATCTAAGTTGTTGAACTGGTCCAAAGGCTACTCGGTAGGTGTTTGTGTTGTT 342
 Db CGTGAAGTGCAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 377

 QY 343 TGCCGCCACCCGGTGCATTCGAGGACACCAACCAATCACCAGTATGACGCAACCTCTAC 402
 Db TACCTGTTTGTGCACTCAAGAACACCGTCCAGTCCGCGTGGGCACTTCCCGCGTCC 317

 QY 403 CAGCACCACCGAAGTTACATCCAGTACGACCCCATATACGTGCCATGTAGTGCCTTAG 462
 Db CTGCGTTGTCGAAGTGCAGTTTGTTCGACCCCGAGATGCTCTCTCTGTCGTCGCTCG 257

 QY 463 GCGCATCAATGACCCACATTTGGCTCTGATCGAGACGTCGGGCAACCGCTATCCGGTCTGA 522
 Db TCAGCTCATGTTCCACGATTCGCGAGGTTAAGCTTGAGCCGCGCGCGGACGCGG- 198

 QY 523 TGCGGCCCAACGATGATGACAGAGTTGTTGGCGGT 558
 Db TCGCGGCCCAACGATGATGACAGAGTTGTTGGCGGT 163

RESULT 13
 US-10-165-165-389/c
 ; Sequence 389, Application US/10259165
 ; Publication No. US20030135888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; APPLICANT: Chang, Hur-song
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiyaki
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Moughamer, Todd
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Ricke, Darrell

;; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING

;; FILE REFERENCE: 70030-NP
 ;; CURRENT APPLICATION NUMBER: US/10/259,165
 ;; CURRENT FILING DATE: 2002-09-26
 ;; PRIOR APPLICATION NUMBER: US 60/370,620
 ;; PRIOR FILING DATE: 2002-04-04
 ;; PRIOR APPLICATION NUMBER: US 60/368,327
 ;; PRIOR FILING DATE: 2002-03-27
 ;; PRIOR APPLICATION NUMBER: US 60/325,277
 ;; PRIOR FILING DATE: 2001-09-26
 ;; NUMBER OF SEQ ID NOS: 782
 ;; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
 ;; SEQ ID NO 389
 ;; LENGTH: 717
 ;; TYPE: DNA
 ;; ORGANISM: Oryza sativa
 US-10-259-165-389

Query Match 8.6%; Score 136.8; DB 15; Length 717;
 Best Local Similarity 58.8%; Pred. No. 3.9e-20;
 Matches 274; Conservative 0; Mismatches 187; Indels 5; Gaps 2;

QY 98 GGTGCAACAATATTTGTTCTCCAAATGTGGTACAGGATTTTACATCTCTCCGGGTAC 157
 DB 541 GGTGCAACAATATTTGTTCTCCAAATGTGGTACAGGATTTTACATCTCTCCGGGTAC 482

QY 158 TTTAAGCTGACTAGGACATTCACCAATTTATTTCCGCTGCATTGAATTGTG---TGGC 213
 DB 481 CCTAGCTGCTCGGGCACTGCCCCCGCCACGTCGCGCCCGCCGCTTGGC 422

QY 214 ATTTCCCTCCATTTGATTAGTCGGGGCGAAAGTCATCGGTATATTAATCAACTA 273
 DB 421 GCACCCGGCGCGCTGCGCGGGGGGAGGAGTCCATGGCAGCTTGAATCCGTCGATGA 362

QY 274 AAGAAATCTCCAGAAATCTAAGTTTGAATCTGTCAGAGCGTCTCAAGCGTACTCGCTAGGTTGT 333
 DB 361 GGGAGATGTCGAAGAAGTCGAGGTTCGTAATCTGTTGAGCGCAACTTCCGCCAGCGTGT 302

QY 334 TTGTGTGTTTGGCCCAACCGGTGCACTGCAGGACACACCAATCAACAGTCATGACAG 393
 DB 301 TGGCGGCTGCGCGTACGCGCGCACCGCAGCAGCGCGCGCGCTGCGCGCTTGGCAC 242

QY 394 AACCTTACAGCAGCAGCAGGATTTACATCAGTACGACCCCATATAGTGCATCGTAG 453
 DB 241 GCGCGTTGCGCGTGCAGTGCAGGTCGAGCGCGTGCAGCGCGCACAGCGCGCGCGCTG 182

QY 454 TGCCCTAGGCGCATCAATGACCCACATTTGGCTCGATCGAGACGTCGGGACCGCCTA 513
 DB 181 TGCGGCGCGCACGTCGATCACCACCTGCTGCCCCGGTCCAGCTGCTGCCCCCGCG 122

QY 514 TCGGCTCG-ATGCGCGCCCAACGATGTATGACAGTTGTTCGCGGT 558
 DB 121 ACGGCACGCGTGGCGCCACACGCGTGTCTGGCACTTGTGGTGAT 76

RESULT 14

US-10-259-165-41/c
 ; Sequence 41, Application US/10259165
 ; Publication No. US20030135888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhu, Tong
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Chang, Hur-song
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiyaki
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Moughamer, Todd
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Ricke, Darrell
 ; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING

;; FILE REFERENCE: 70030-NP
 ;; CURRENT APPLICATION NUMBER: US/10/259,165
 ;; CURRENT FILING DATE: 2002-09-26
 ;; PRIOR APPLICATION NUMBER: US 60/370,620
 ;; PRIOR FILING DATE: 2002-04-04
 ;; PRIOR APPLICATION NUMBER: US 60/368,327
 ;; PRIOR FILING DATE: 2002-03-27
 ;; PRIOR APPLICATION NUMBER: US 60/325,277
 ;; PRIOR FILING DATE: 2001-09-26
 ;; NUMBER OF SEQ ID NOS: 782
 ;; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
 ;; SEQ ID NO 41
 ;; LENGTH: 720
 ;; TYPE: DNA
 ;; ORGANISM: Oryza sativa
 US-10-259-165-41

Query Match 8.6%; Score 136.8; DB 15; Length 720;
 Best Local Similarity 58.8%; Pred. No. 3.9e-20;
 Matches 274; Conservative 0; Mismatches 187; Indels 5; Gaps 2;

QY 98 GGTGCAACAATATTTGTTCTCCAAATGTGGTACAGGATTTTACATCTCTCCGGGTAC 157
 DB 541 GGTGCAACAATATTTGTTCTCCAAATGTGGTACAGGATTTTACATCTCTCCGGGTAC 482

QY 158 TTTAAGCTGACTAGGACATTCACCAATTTATTTCCGCTGCATTGAATTGTG---TGGC 213
 DB 481 CCTAGCTGCTCGGGCACTGCCCCCGCCACGTCGCGCCCGCCGCTTGGC 422

QY 214 ATTTCCCTCCATTTGATTAGTCGGGGCGAAAGTCATCGGTATATTAATCAACTA 273
 DB 421 GCACCCGGCGCGCTGCGCGGGGGGAGGAGTCCATGGCAGCTTGAATCCGTCGATGA 362

QY 274 AAGAAATCTCCAGAAATCTAAGTTTGAATCTGTCAGAGCGTCTCAAGCGTACTCGCTAGGTTGT 333
 DB 361 GGGAGATGTCGAAGAAGTCGAGGTTCGTAATCTGTTGAGCGCAACTTCCGCCAGCGTGT 302

QY 334 TTGTGTGTTTGGCCCAACCGGTGCACTGCAGGACACACCAATCAACAGTCATGACAG 393
 DB 301 TGGCGGCTGCGCGTACGCGCGCACCGCAGCAGCGCGCGCGCTGCGCGCTTGGCAC 242

QY 394 AACCTTACAGCAGCAGCAGGATTTACATCAGTACGACCCCATATAGTGCATCGTAG 453
 DB 241 GCGCGTTGCGCGTGCAGTGCAGGTCGAGCGCGTGCAGCGCGCACAGCGCGCGCGCTG 182

QY 454 TGCCCTAGGCGCATCAATGACCCACATTTGGCTCGATCGAGACGTCGGGACCGCCTA 513
 DB 181 TGCGGCGCGCACGTCGATCACCACCTGCTGCCCCGGTCCAGCTGCTGCCCCCGCG 122

QY 514 TCGGCTCG-ATGCGCGCCCAACGATGTATGACAGTTGTTCGCGGT 558
 DB 121 ACGGCACGCGTGGCGCCACACGCGTGTCTGGCACTTGTGGTGAT 76

RESULT 15

US-10-437-963-86607/c
 ; Sequence 86607, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 05:06:40 ; Search time 3757.1 Seconds
(without alignments)
12701.209 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum.*
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5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_est3.*
12: gb_est4.*
13: gb_est5.*
14: gb_est6.*
15: em_estfun.*
16: em_estom.*
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18: em_gss_inv.*
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20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	474.6	29.7	899	14	CK252883
c 2	474.6	29.7	1004	14	CK248798
c 3	471.4	29.5	988	14	CK246326
c 4	469.6	29.4	888	14	CK278032

c 5	469	29.3	853	14	CK271811	CK271811 EST17889
c 6	468.6	29.3	899	14	CK252271	CK252271 EST735908
c 7	465.2	29.1	739	12	BI176339	BI176339 EST521129
c 8	456.6	28.6	649	9	AW039873	AW039873 EST282345
c 9	455.2	28.5	583	12	BI432833	BI432833 EST535594
c 10	451.6	28.3	639	12	BG130690	BG130690 EST463582
c 11	449.6	28.1	667	12	BI922472	BI922472 EST542376
c 12	449	28.1	622	10	BF053678	BF053678 EST438908
c 13	447.2	28.0	585	9	AW031249	AW031249 EST274624
c 14	440.8	27.6	583	9	AW032915	AW032915 EST276474
c 15	439.2	27.5	933	14	CK273930	CK273930 EST720008
c 16	439	27.5	649	10	AW222204	AW222204 EST299015
c 17	439	27.5	652	12	BI921170	BI921170 EST541073
c 18	439	27.5	669	12	BI921735	BI921735 EST541638
c 19	439	27.5	782	12	BM410787	BM410787 EST585114
c 20	438.8	27.5	598	14	CA514039	CA514039 KS09015D0
c 21	437.8	27.4	651	10	AW218785	AW218785 EST301265
c 22	436.8	27.3	777	12	BM407898	BM407898 EST582225
c 23	435.8	27.3	586	9	AW033588	AW033588 EST27159
c 24	431.8	27.0	944	14	CK271145	CK271145 EST717223
c 25	430	26.9	657	10	AW223507	AW223507 EST300318
c 26	427.4	26.7	936	14	CK277819	CK277819 EST723897
c 27	426.8	26.7	575	12	BI421330	BI421330 EST531996
c 28	426.6	26.7	629	10	BE432710	BE432710 EST399239
c 29	425.8	26.6	574	10	AW441774	AW441774 EST311170
c 30	425.8	26.6	776	12	BG123560	BG123560 EST469306
c 31	425.8	26.6	916	14	CK279273	CK279273 EST725351
c 32	425.6	26.6	638	12	BI434454	BI434454 EST537215
c 33	425.6	26.6	757	12	BI434095	BI434095 EST536856
c 34	425	26.6	604	12	BI423179	BI423179 EST533845
c 35	425	26.6	637	12	BI921311	BI921311 EST541214
c 36	425	26.6	719	12	BI422260	BI422260 EST532926
c 37	425	26.6	720	12	BI921826	BI921826 EST541729
c 38	425	26.6	807	12	BI421946	BI421946 EST532612
c 39	424.2	26.5	574	10	AW223623	AW223623 EST300434
c 40	424	26.5	626	9	AW033829	AW033829 EST277400
c 41	423	26.5	682	10	AW223970	AW223970 EST300781
c 42	423	26.5	710	9	AW035171	AW035171 EST280433
c 43	422.8	26.5	573	9	AW032317	AW032317 EST275771
c 44	422.4	26.4	660	12	BM403979	BM403979 EST578306
c 45	421.6	26.4	626	12	BI421167	BI421167 EST531833

ALIGNMENTS

RESULT 1
CK252883/c 899 bp mRNA linear EST 12-DEC-2003
LOCUS
DEFINITION
EST736520 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POC086 5' end, mRNA sequence.
ACCESSION
CK252883
VERSION
CK252883.1 GI:39807285
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 899)
AUTHORS
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
TITLE
Generation of ESTs from potato callus tissue
JOURNAL
Unpublished (2003)
COMMENT
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: Arr TAG GTG ACA CTA TAG.

FEATURES
source
1..899
/organism="Solanum tuberosum"
/mol_type="mRNA"

/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POC086"
/tissue="callus"
/lab_host="DH10B-Tona"
/clone_lib="potato callus cDNA library, normalized and full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

ORIGIN

Query Match 29.7%; Score 474.6; DB 14; Length 899;
Best Local Similarity 88.2%; Pred. No. 1.5e-88;
Matches 539; Conservative 0; Mismatches 69; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACACATGGACCTTGGGTGCAAC 105
DB 611 GGCATCTTTGTTGAAAAATCTAGCAAAATCAGTAGGCCACATGGACCTTGGGTGCAAC 552

QY 106 AATATGTTGTCCTCCAAATGTGTACAAAGATTGTACATCTCCCGGTACTTTAAGCT 165
DB 551 AATATGTTGTCCTCCGAACTGTGTACAAAGATTGTACATCTCCCGGTACTTTAAGCT 492

QY 166 GACTAGGACATTCACATTTATATTGCGGTGCAATGAAATGTTGTCGCAATTCCTCCAC 225
DB 491 AACAGGACATTCACATTTATATTAGCGGTGCAATGAAATGTTGTCGCAATTCCTCCAC 432

QY 226 TTGGATTAGTCGGGCGGAAAGTCATCGGTATATTAATTCATCAATCAAGAAATGTC 285
DB 431 TAGGATTGTTGGGCGGAAAGTCATCGGTATATTAATTCATCAATCAAGAAATGTC 372

QY 286 AGAATCTAAGTTGTTGAACTGTTCCAGGCGTACTCGGTAGGCTTTGGTGGTTGC 345
DB 371 AGAATCTAAGTTGTTGAACTGTTCCAGGCGTACTCGGTAGGCTTTGGTGGTTGC 312

QY 346 CCCACCCCGTCACTGACGAGCACACACCAATCACCAGTCATGACGAACTCTACAC 405
DB 311 CCCACCCGTACATGCAAGACCCACCAATCACCAGTCGCAATGAACTCTACAC 252

QY 406 CACACCGAAGTTACATCCAGTACGACCCATATACGTGCGCATGTAGTCCCGTAGGCG 465
DB 251 CACCATCAAGTTGCAATAGTACGACCCCATATACGTGCGCATGTAGTCCCGTAGGCG 192

QY 466 CATCAATCACCACATTTGGGCTCGATCGAGACGTGCGGCAACCCCTATC -GGGTGCGATG 524
DB 191 CATGATAACCCATGCTGGGCTCGATCGAGACGTGCGGCAACCCCTATC -GGGTGCGATG 132

QY 525 CGGCCCCAAGCATGTATGACAGTTGTTGGCGGTACCTCGCATAGTGAAGTAAAGTAA 584
DB 131 CGGCCCCAAGCATGTATGACAGTTAATG -CGTACCTCGCATAGTGAAGTAAAGTAA 74

QY 585 AGTCACAAAGCCAGAGGAGAAACCAAGAGAGTCTCAAGTAGCCCATGTTGTTGA 644
DB 73 AGTCACAAAGCCAGAGGAGAAACCAAGAGAGTCTCAAGTAGCCCATGTTGTTGA 14

QY 645 AATTTATATGT 655
DB 13 ACTATATTTT 3

RESULT 2
CK248798/c
LOCUS
DEFINITION
EST732435 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POCB364 5' end, mRNA sequence.
CK248798
ACCESSION
CK248798.1 GI:39799290
EST.
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 1004)
Buell, C.R., Hart, A., Zismann, V., Karameycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1..1004
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POC364"
/tissue="callus"
/lab_host="DH10B-Tona"
/clone_lib="potato callus cDNA library, normalized and full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

ORIGIN

Query Match 29.7%; Score 474.6; DB 14; Length 1004;
Best Local Similarity 88.2%; Pred. No. 1.5e-88;
Matches 539; Conservative 0; Mismatches 69; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACACATGGACCTTGGGTGCAAC 105
DB 610 GGCATCTTTGTTGAAAAATCTAGCAAAATCAGTAGGCCACATGGACCTTGGGTGCAAC 551

QY 106 AATATGTTGTCCTCCAAATGTGTACAAAGATTGTACATCTCCCGGTACTTTAAGCT 165
DB 550 AATATGTTGTCCTCCGAACTGTGTACAAAGATTGTACATCTCCCGGTACTTTAAGCT 491

QY 166 GACTAGGACATTCACATTTATATTGCGGTGCAATGAAATGTTGTCGCAATTCCTCCAC 225
DB 490 AACAGGACATTCACATTTATATTAGCGGTGCAATGAAATGTTGTCGCAATTCCTCCAC 431

QY 226 TTGGATTAGTCGGGCGGAAAGTCATCGGTATATTAATTCATCAATCAAGAAATGTC 285
DB 430 TAGGATTGTTGGGCGGAAAGTCATCGGTATATTAATTCATCAATCAAGAAATGTC 371

QY 286 AGAATCTAAGTTGTTGAACTGTTCCAGGCGTACTCGGTAGGCTTTGGTGGTTGC 345
DB 370 AGAATCTAAGTTGTTGAACTGTTCCAGGCGTATTCAGCCAGGGGTGTTGGTGGTTGC 311

QY 346 CCCACCCGTGACATGACGAGCACACCAATCACCAGTCATGACGAACTCTTACAC 405
DB 310 CCCACCCGTACATGCAAGACCCACCAATCACCAGTCATGCAATCACTCTACAC 251

QY 406 CACACCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATGTAGTCCCGTAGGCG 465
DB 250 CACCATCAAGTTGCAATTAGTACGACCCCATATACGTGCGCATGTAGTCCCGTAGGCG 191

QY 466 CATCAATCACCACATTTGGGCTCGATCGAGACGTGCGGCAACCCCTATC -GGGTGCGATG 524
DB 190 CATGATAACCCATGCTGGGCTCGATCGAGACGTGCGGCAACCCCTATC -GGGTGCGATG 131

QY 525 CGGCCCCAAGCATGTATGACAGTTGTTGGCGGTACTCTCGATAGTGAAGTAAAGTAA 584
DB 130 CGGCCCCAAGCATGTATGACAGTTAATG -CGTACCTCGCATAGTGAAGTAAAGTAA 73

QY 585 AGTCACAAAGCCAGAGGAGAAACCAAGAGAGTCTCAAGTAGCCCATGTTGTTGA 644
DB 72 AGTCACAAAGCCAGAGGAGAAACCAAGAGAGTCTCAAGTAGCCCATGTTGTTGA 13

QY 645 AATTTATATGT 655
DB 13 ACTATATTTT 1

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Db      12 ACTATATTTTT 2

RESULT 3
CK246326/c
LOCUS      988 bp      mRNA      linear      EST 12-DEC-2003
DEFINITION EST729963 potato callus cDNA library, normalized and full-length
            Solanum tuberosum cDNA clone POCAL08 5' end, mRNA sequence.
ACCESSION  CK246326
VERSION     CK246326.1 GI:39793747
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
ORGANISM    Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE   1 (bases 1 to 988)
AUTHORS    Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
TITLE      Generation of ESTs from potato callus tissue
JOURNAL    Unpublished (2003)
COMMENT    Other ESTs: EST729964
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            Seq primer: Ant TAG GTG ACA CTA TAG.

FEATURES             source
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            /db_xref="taxon:4113"
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            /tissue_type="callus"
            /lab_host="DH10B-TonA"
            /clone_lib="potato callus cDNA library, normalized and
            full-length"
            /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
            supplier: RNA was isolated from Solanum tuberosum var.
            Kennebec callus tissue grown on solid media."

ORIGIN
Query Match      29.5%; Score 471.4; DB 14; Length 988;
Best local Similarity 88.6%; Pred. No. 5.9e-86;
Matches 534; Conservative 0; Mismatches 56; Indels 3; Gaps 2;

Qy      46  GGTATCTTTGTTGAAAAAATTGGAAGAAGACGTAGGACACATGCGACCTTGGGTGCAAC 105
Db      601 GGCATCTTTGTTGAAAAAATCTAGACAAATCAGTAGGACACATGCGACCTTGGGTGCAAC 542

Qy      106 AATATTGTTGCTCCCAATGTTGACAGGAATTTACATCTCCGGGTACTTTAAGCT 165
Db      541 AATATTGTTGCTCCGAACTGTTGACAGGAATTTGTTACATCTCCAGGTACCTTAAGT 482

Qy      166 GACTAGGACATTCACCATTTATTTGCGGTGCAATGAAATTTGTGTGCAATTCCTCCAC 225
Db      481 AACGAGNATTCACCATTTATATTAGCCGTGCAATGAAATTTGCGGTGCAATTCCTCCAC 422

Qy      226 TTGATAGTCGGGGCGAAAGTCATGCGTATTTAAATTCATCACTAAAGAAATGCCC 285
Db      421 TAGGATTTGTTGGGCGAAAAGTCATCGGAATTTAAATTCATCGACTAAAGAAATGCCC 362

Qy      286 AGAATCTTAAGTTCTGAACCTGTTCCAGGGGTACTCGGTAGGCTTTGTTGGTTTC 345
Db      361 AGAATCTTAAGTTCTGAACCTGTTCCAGGGGTACTCGGTAGGCTTTGTTGGTTTC 302

Qy      346 CCCACCGGGTCACTGAGGACACACCAATCACCAGTCATGACGAACTCTACAG 405
Db      301 CCCACCGGGTCACTGAGGACACACCAATCACCAGTCATGACGAACTCTACAG 242

Qy      406 CACCACCGAAGTTACATCCAGTAGACCCCATATACGTGCATCGTAGTCCCTTAGCG 455

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Db      241 CACCATCAAAAGTTGCAATTAGTAGCACCACCATATACGTGCATCTTAGTGCCTCCGGCG 182
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Db      181 CATGTATAACCCATGTCTGGCTCGATCGAGAGCTGGGACCGCTATGCGGGTGGATG 122
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Qy      525 CCSCCCAAACGATGTATGACAGCTTGTTCGGCGTACTCGATAGTCAGACGATCAAGTGA 584
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Db      121 CGCCCCACACGGTGTATGACAGTATTG-CGTACTCGATAGTGGCAGCATAGTGA 64
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Qy      585 AGTCACAAAGCCAGAGGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGA 644
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Db      63 AGTCACAAAGCAAGGAGGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGA 4
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Qy      645 AAT 647
            |||
            |||
Db      3 ACT 1

RESULT 4
CK278032/c
LOCUS      888 bp      mRNA      linear      EST 12-DEC-2003
DEFINITION EST724110 potato abiotic stress cDNA library Solanum tuberosum cDNA
            clone POAE351 5' end, mRNA sequence.
ACCESSION  CK278032
VERSION     CK278032.1 GI:39835010
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
ORGANISM    Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE   1 (bases 1 to 888)
AUTHORS    Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
TITLE      Generation of ESTs from abiotic stressed potato tissue
JOURNAL    Unpublished (2003)
COMMENT    Other ESTs: EST724111
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            Clones can be requested from TIGR via potato@tigr.org
            Seq primer: Ant TAG GTG ACA CTA TAG.

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            /clone="POAE351"
            /tissue_type="abiotic stress treated leaf and root tissue"
            /clone_lib="potato abiotic stress cDNA library"
            /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
            supplier: Solanum tuberosum var. Kennebec plants were
            grown from cuttings on a 16hr light/8 hr dark cycle at 25
            C for 3-4 weeks. Abiotic stress conditions were applied to
            four separate sets of plants. Set 1 involved saturation of
            the soil with 150 mM NaCl and tissues were harvested at
            following application of the salt stress (leaves: 2hr,
            6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
            Set 2 were grown under the standard conditions and then
            were water stressed by withdrawal of further watering
            applications. Brought stressed plants were harvested after
            cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
            and 5d). Set 3 were grown under the standard conditions
            and then were cold stressed by placement at 4 C. Cold
            stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
            and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
            and 4d were grown under the standard conditions and
            then were heat stressed by placement at 35 C. Heat
            stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
            2d and 4d and heat-stressed roots were harvested at 6 hr,

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12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

```

ORIGIN
Query Match      29.4%; Score 469.6; DB 14; Length 888;
Best Local Similarity 88.8%; Pred. No. 1.7e-87;
Matches 531; Conservative 0; Mismatches 64; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATTTGAAAGAGACGTAGGACACATGGACCTTGGGTGCAAC 105
DB 597 GGCATCTTTGTTGAAAAAATCTGACAAATCAGTAGGACACATGGACCTTGGGTGCAAC 538

QY 106 AATATTTGTCCTCCAAATGTGTACAAAGATTGTACATCCTCCGGGTACTTTAAGCT 165
DB 537 AATATTTGTCCTCCGAAACGTGTACAAAGATTGTACATCCTCCGGGTACTTTAAGCT 478

QY 166 GACTAGGACATTCACCATTTATTTGCGGTGCAATTCGATTCCTCAATCAATCAATCAAT 225
DB 477 AACCAGGACATTCACCATTTATTTAGCCGTGCAATTCGATTCCTCAATCAATCAATCAAT 418

QY 226 TTGGATTAGTCGGGGCGAAAGTCATCGGTATTTAAATFCCATCAACTAAAGAAATGTCC 285
DB 417 TAGGATTGTTGGGGCGAAAGTCATCGGAATTTAAATFCCATCAACTAAAGAAATGTCC 358

QY 286 AGAATCTTAAGTTGTTGAACCTGGTCCAAAGCGGTACTCGGCTAGGGTGTTCGGTGTTC 345
DB 357 AGAATCTTAAGTTGTTGAACCTGGTCCAAAGCGGTACTCGGCTAGGGTGTTCGGTGTTC 298

QY 346 CCCACCCCGTGCATCTGACGAGCACACCAACCAATCACCAGTCATGACGAACTCTTACCAG 405
DB 297 CCCACCCCGTGCATCTGACGAGCACACCAACCAATCACCAGTCATGACGAACTCTTACCAG 238

QY 406 CACCAACCGAAGTTACATCCAGTACGACCCCATATACGTGECATCGTAGTCCCTTAGCGG 465
DB 237 CACCAATCAAAGTTGCAATTTAGTACGACCCCATATACGTGECATCGTAGTCCCTTAGCGG 178

QY 466 CATCAATGACCCACATTTTGGCTCGATCGAGACGTGCGGGCACCCGCTATC-GGGTCCGATG 524
DB 177 CATGATTAACCATGCTCTGGCTCGATCGAGACGTGCGGGCACCCGCTATC-GGGGTCCGATG 118

QY 525 CGGCCCAACCGAAGTTGTTGCGGTGCAATTCGATTCCTCAATCAATCAATCAATCAAT 584
DB 59 AGTCAAAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60

QY 585 AGTCAAAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 642
DB 59 AGTCAAAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2

```

RESULT 5
CK271811/c
LOCUS
DEFINITION
EST17889 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAD143 5' end, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (Bases 1 to 853)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST17890
Contact: Robin Buell

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
source

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1..853
Location/Qualifiers
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAD143"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d. Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."
```

ORIGIN

```

Query Match      29.3%; Score 469; DB 14; Length 853;
Best Local Similarity 88.6%; Pred. No. 2.3e-87;
Matches 531; Conservative 0; Mismatches 65; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATTTGAAAGAGACGTAGGACACATGGACCTTGGGTGCAAC 105
DB 597 GGCATCTTTGTTGAAAAAATCTGACAAATCAGTAGGACACATGGACCTTGGGTGCAAC 538

QY 106 AATATTTGTCCTCCAAATGTGTACAAAGATTGTACATCCTCCGGGTACTTTAAGCT 165
DB 537 AATATTTGTCCTCCGAAACGTGTACAAAGATTGTACATCCTCCGGGTACTTTAAGCT 478

QY 166 GACTAGGACATTCACCATTTATTTGCGGTGCAATTCGATTCCTCAATCAATCAATCAAT 225
DB 477 AACCAGGACATTCACCATTTATTTAGCCGTGCAATTCGATTCCTCAATCAATCAATCAAT 418

QY 226 TTGGATTAGTCGGGGCGAAAGTCATCGGTATTTAAATFCCATCAACTAAAGAAATGTCC 285
DB 417 TAGGATTGTTGGGGCGAAAGTCATCGGAATTTAAATFCCATCAACTAAAGAAATGTCC 358

QY 286 AGAATCTTAAGTTGTTGAACCTGGTCCAAAGCGGTACTCGGCTAGGGTGTTCGGTGTTC 345
DB 357 AGAATCTTAAGTTGTTGAACCTGGTCCAAAGCGGTACTCGGCTAGGGTGTTCGGTGTTC 298

QY 346 CCCACCCCGTGCATCTGACGAGCACACCAACCAATCACCAGTCATGACGAACTCTTACCAG 405
DB 297 CCCACCCCGTGCATCTGACGAGCACACCAACCAATCACCAGTCATGACGAACTCTTACCAG 238

QY 406 CACCAACCGAAGTTACATCCAGTACGACCCCATATACGTGECATCGTAGTCCCTTAGCGG 465
DB 237 CACCAATCAAAGTTGCAATTTAGTACGACCCCATATACGTGECATCGTAGTCCCTTAGCGG 178

QY 466 CATCAATGACCCACATTTTGGCTCGATCGAGACGTGCGGGCACCCGCTATC-GGGTCCGATG 524
DB 177 CATGATTAACCATGCTCTGGCTCGATCGAGACGTGCGGGCACCCGCTATC-GGGGTCCGATG 118

QY 525 CGGCCCAACCGAAGTTGTTGCGGTGCAATTCGATTCCTCAATCAATCAATCAATCAAT 584

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Db 117 CGCCCCACACGGTGTATGACAGTTATTG--CGTACCTCGATAGTGGCAGCATAAAGTGA 60

Qy 585 AGTCACAAAGCGAGAGGAGAAACCAAGAGAGATCTCAAGTAGCCCAATGTTTGTG 643

Db 59 AGTCACAAAGCGAGAGGAGAGAAACCAAGAGAGATCTCAAGTAGCCCAATGTTTGTG 1

RESULT 6
CK252271/c
LOCUS
DEFINITION
EST735908 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POCB787 5' end, mRNA sequence.

ACCESSION
CK252271
VERSION
CK252271.1 GI:39806102
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)

REFERENCE
AUTHORS
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE
Generation of ESTs from potato callus tissue
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: EST735909
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
source
Location/Qualifiers
1..899
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCB787"
/tissue_type="callus"
/lab_host="DHI0B-Tona"
/clone_lib="potato callus cDNA library, normalized and full-length"
/note="Vector: pCW9Sport6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

ORIGIN
Query Match 29.3%; Score 468.6; DB 14; Length 899;
Best Local Similarity 88.8%; Pred. No. 2.7e-87;
Matches 530; Conservative 0; Mismatches 64; Indels 3; Gaps 2;

Qy 46 GGTATCTTTGTTTGAAGAAATGGAAGACGTAGGACCAACATGGACCTTGGTGCAAC 105

Db 596 GGCATCTTTGTTTGAAGAAATGACAAATCAGTAGGACCAATGGACCTTGGTGCAAC 537

Qy 106 AATATTGTTGCTCCCAATGTTGTACAGGATTGTTACATCCCGGGTACTTTAAGCT 165

Db 536 AATATTGTTGCTCCCGACGTGTGTACAGGATTGTTACATCCCGAGGTACCCTAAGT 477

Qy 166 GACTAGACATTCACATTTATATTGCGGTGCAATGAATGTGTGCAATTCCTCCAC 225

Db 476 AACCAGGACATTCACCAATTTATATTAGCGGTGCAATGAATGTGTGCAATTCCTCCAC 417

Qy 226 TTGATTAGTCGGGGCGAAGTCATCGGTATTTAAATCCATCACTAAGAAATGTCCTC 285

Db 416 TAGAATGTTGGGGCGAAGTCATCGGTATTTAAATCCATCACTAAGAAATGTCCTC 357

Qy 286 AGAAATCTAAGTTGTTGAACGTGTCCTCAAGGCGTACTCGGTAGGGTGTGTTGGTTGC 345

Db 356 AGAAATCTAAGTTGTTGCTGAACGTGTCCTCAAGGCGTATTTCAGCCAGGGTGTGTTGGTTGC 297

Qy 346 CCCACCCGGTGCACTGCGAGCACCAACCAATCACCAGTCATGCGACCACTCTACCAG 405

Db 296 CCACCCGGTACACTGCAAGACCCACCAATCACCAGTCTCGCATGAACCTCTACCAG 237

Qy 406 CACACCGAAGTTACATCCAGTACGACCCCATATAGTCCCATCTAGTCCCTAGGCG 465

Db 236 CACCATCAAGTTGCAATTAGTACGACCCCATATAGTCCCATCTAGTCCCTAGGCG 177

Qy 466 CATCAATGACCCACATTTGGCCCTCGATCGAGACGTGGGCGACCGCTATC-GGGTGGATG 524

Db 176 CATTGATAACCCATGTCGGCTCGATCGAGAGCTGGCCACCGCTATCGGGGTGATG 117

Qy 525 CCSCCCAAAGCATGTATGGACAGTTTGGCGGTACTCGATAGTACAGCATATAAGTAA 584

Db 116 CCSCCCACACGGTGTATGGACAGTTATTG--CGTACCTCGATAGTGGCAGCATAAAGTGA 59

Qy 585 AGTCACAAAGCGAGAGGAGAGAAACCAAGAGATCTCAAGTAGCCCAATGTTGT 641

Db 58 AGTCACAAAGCGAGAGGAGAGAAACCAAGAGATCTCAAGTAGCCCAATGTTGT 2

RESULT 7
Bil176339/c
LOCUS
DEFINITION
EST521129 P. infestans-challenged potato leaf, compatible reaction
Solanum tuberosum cDNA clone PFCAC11 5' sequence similar to osmotin-like protein {Capsicum annum}, mRNA sequence.

ACCESSION
Bil176339
VERSION
Bil176339.1 GI:14642150
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)

REFERENCE
AUTHORS
Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E. and Baker, B.
TITLE
Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.

FEATURES
source
Location/Qualifiers
1..739
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PFCAC11"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLP"
/clone_lib="P. infestans-challenged potato leaf, compatible reaction"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University, Fry lab; sequencing: The Institute for Genomic Research; Whole plants were challenged with 20,000 sporangia/ml of the compatible P. infestans isolate US 940480. Leaf tissue was collected at 3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed first symptoms of infection at 48 hours after inoculation. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."

ORIGIN

Query Match 29.1%; Score 465.2; DB 12; Length 739;
 Best Local Similarity 88.9%; Pred. No. 1.4e-86;
 Matches 526; Conservative 0; Mismatches 63; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTTGAAGAAATTTGAAAGAAAGTGGAGGACACATGAGACCTTGGGTGCAAC 105
 DB 590 GGATCTTTGTTTGAAGAAATTTGAAAGAAATTCACAAATCAGTAGGACACATGAGCTTGGTGCAC 531

QY 106 AATATGTTGTCCTCAAAATGTTGTAACAAGATGTTTACATCTCTCCGGGTACTTTAAGCT 165
 DB 530 AATATGTTGTCCTCCGAACGTGTACAAGATGTTTACATCTCTCCAGGTACCTAAGTG 471

QY 166 GACTAGGACATTCACATTTATATTTCCGCTGCAATGAATGTTGTCATTTCCCTCCAC 225
 DB 470 AACGAGACATTCACATTTATATTTAGCCGTGCATGAATGCTGACATTTCCCTCCAC 411

QY 226 TTGATTAGTCGGGGCGAAAGTCACTCGGTATATTTAAATCCATCAACTAAAGAAATGTCCC 285
 DB 410 TAGGATTGTTGGGCGAAAGTCACTCGGAATATTTAAATCCATCAACTAAAGAAATGTCCC 351

QY 286 AGAATCTAAGTTGTTGAACTGTTCCAAAGGCTACTCGGTAGGTTTGGTGGTTTC 345
 DB 350 AGAATCTAAGTTGTTGAACTGTTCCAAAGGCTACTCGGTAGGTTTGGTGGTTTC 291

QY 346 CCCACCCGGTGCATCGAGGACACACCAATCACCAGTCATGCACGAACCTCTACCAG 405
 DB 290 CCCACCCGGTACATTCAGAGCCCAACCAATCACCAGTTTGCATGAACCTCTGCCAG 231

QY 406 CACACCGAAGTTCATCCAGTACGACCCCAATATAGTGCATCTGTAAGTCCCTTAGCGG 465
 DB 230 CACCATCAAGTTCAATTTAGTACGACCCCAATATAGTGCATCTGTAAGTCCCTTAGCGG 171

QY 466 CATCAATGACCCCATTTGGCTCGATCGAGCTGCGGACCGCCCTATC-GGTCGATG 524
 DB 170 CATGATGACCCCATTTGGCTCGATCGAGCTGCGGACCGCCCTATC-GGTCGATG 111

QY 525 CCGCCCAACGATGATGACAGTTGTTGGCGTACCTCGATAGTACGACATAGTGAA 584
 DB 110 CCGCCCAACGATGATGACAGTTGTTG--CGTACCTCGATAGTACGACATAGTGAA 53

QY 585 AGTCACAAAGCCAGAGGAGAAACAAAGAGATCTCAAGTACCCATG 636
 DB 52 AGTCACAAAGCCAGAGGAGAAACAAAGAGATCTCAAGTACCCATG 1

RESULT 8
 AW039873/c
 LOCUS
 DEFINITION EST282346 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET13J13, mRNA sequence.
 ACCESSION AW039873
 VERSION AW039873.1 GI:5898627
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum

REFERENCE
 AUTHORS
 Giovannoni, J.
 Generation of ESTs from tomato leaf tissue
 Unpublished (1999)
 CONTACT CUGI
 CLEMSON UNIVERSITY
 CLEMSON UNIVERSITY
 100 JORDAN HALL, CLEMSON, SC 29634, USA
 EMAIL: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.
 LOCATION/Qualifiers
 1. .649

RESULT 9
 BI432833/c
 LOCUS
 DEFINITION EST535594 P. infestans-challenged potato leaf, compatible reaction Solanum tuberosum cDNA clone PPCAW35 5' sequence, mRNA sequence.
 ACCESSION BI432833
 VERSION BI432833.1 GI:15257523
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

/organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="Rio Grande PtoR"
 /db_xref="taxon:4081"
 /clone="cLET13J13"
 /tissue_type="leaf"
 /dev_stage="4-6 week old plants"
 /lab_host="XLI-Blue MRF"
 /clone_lib="tomato mixed elicitor, BTI"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; cJET - inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotin acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

ORIGIN

Query Match 28.6%; Score 456.6; DB 9; Length 649;
 Best Local Similarity 87.9%; Pred. No. 9.2e-85;
 Matches 521; Conservative 0; Mismatches 69; Indels 3; Gaps 2;

QY 49 ATCTTTGTTTGAAGAAATTTGAAAGAAAGTGGAGACACATGAGACCTTGGGTGCAACAT 108
 DB 591 ATCTTTGTTTGAAGAAATTTGAAAGAAATTCGACAAATCAGTAGGCGCACATGAGACCTTGTGTGCAACAT 532

QY 109 ATTGTTGTCCTCCAAATGTTGTACAAAGATTTGTACATCTCTCCGGGTACTTTAAGCTGAC 168
 DB 531 ATTGTTGTCCTCCGAACTGTTGTACAAAGATTTGTACATCTCTCCGGGTACTTTAAGTGAAC 472

QY 169 TAGGACATTCACCAATTTATTTCCGTCGATTTGAAATTTGTGTGTCATTTCCCTCCACTTG 228
 DB 471 CAGGACATTCACCAATTTATTTAGCCGTACAAATGAAATTTGCAATGTCATTTCCCTCCACTTG 412

QY 229 GATTAGTCGGGGCGAAAGTCACTCGGTATATTTAAATTCATCAACTAAAGAAATGTCCAGA 288
 DB 411 GATTAGTCGGGGCGAAAGTCACTCGGTATATTTAAATTCATCAACTAAAGAAATGTCCAGA 352

QY 289 AATCTAAGTTGTTGAATCTGGTCCAAAGCGTACTCGGTAGGTTGTTGGTGGTTGCCCC 348
 DB 351 AATCTAAGTTGTTGAATCTGGTCCAAAGCGTACTCGGTAGGTTGTTGGTGGTTGCCCC 292

QY 349 ACCCGTCGATCGAGGACACCAATCACCAGTCATCAGCAACCTCTACAGCAC 408
 DB 291 ACCCGTCGATCGAGGACACCAATCACCAGTCATCAGCAACCTCTACAGCAC 232

QY 409 CACCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCTAGTGCCTTAGCGCGAT 468
 DB 231 CATCAAGTTGCAATTCGTACGACCCCATATACGTGCGCATCTAGTGCCTTAGCGCGAT 172

QY 469 CAATGACCCCATTTGGCTCGATCGAGACCTCGGGACCGCCTA-TCGGGTGCGATCCG 527
 DB 171 TGATGACCCCATTTGGCTCGATCGAGACCTCGGGACCGCCTA-TCGGGTGCGATCCG 112

QY 528 CCCAAACGATGTATGACAGTTGTTGGCGGTACTCTCGATAGTGCAGCATTAAGTGAAGT 587
 DB 111 CCCGACCGGTGTATGACAGTTGTTG--CGTACCTCGAAAGTGGCAGCATTAAGTGAAGT 54

QY 588 CACAAAGCCGAGAGGAGAAACCAAGAGATCTCAAGTAGGCCATGTTTG 640
 DB 53 CACAAAGCCGAGAGGAGAAACCAAGAGATCTCAAGTAGGCCATGTTTG 1

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 583)
 Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemiango, A., Bougri, O., Buell, C.R., Renning, C.M., Fry, W.E. and Baker, B.
 Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction
 Unpublished (2000)
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
<http://genome.arizona.edu/orders/>
 Seq primer: M13F-R.

FEATURES

1. 583
 Location/Qualifiers
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="PPCAM35"
 /tissue_type="leaf"
 /dev_stage="6 week old"
 /lab_host="SOLR"
 /clone_lib="P. infestans-challenged potato leaf, compatible reaction"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University, Fry lab; sequencing: The Institute for Genomic Research; Whole plants were challenged with 20,000 sporangia/ml of the compatible P. infestans isolate US 940480. Leaf tissue was collected at 3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed first symptoms of infection at 48 hours after inoculation. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."

ORIGIN

Query Match 28.5%; Score 455.2; DB 12; Length 583;
 Best Local Similarity 88.7%; Pred. No. 1.8e-84;
 Matches 516; Conservative 0; Mismatches 63; Indels 3; Gaps 2;
 57 TGGAAAGACGTAGGACCATGGACCTTGGGTGCAACATATTTGTCTTCCAATG 126
 581 TCGACAAATAGTAGGACCATGGACCTTGGGTGCAACATATTTGTCTTCCAATG 522
 127 TGGTACAGGATTTACATCTCCGGGTACTTTTAAAGTCACTAGGACATTCACCATTTA 186
 521 TGGTACAGGATTTACATCTCCAGTACCTTAAGTGAACAGGACATTCACCATTTA 462
 187 TATTGCGGTGCATGAATTTGTGGGATTTCCCTCACTTGGATTTAGTCGGGCGAAG 246
 461 TATTAGCGTGCAATGAATTCGTGACATTTCCCTCCACTAGGATTTGGGGCGAAG 402
 247 TCATCGGTATATTAATCCATCACTAAGAAATGTCCAGAAATCAAGTTGTGAAT 306
 401 TCATCGGATATTAATCCATCGACTAAGAAATGTCCAGAAATCAAGTTGTGAAT 342
 307 GGTCCAGCGTACTCGGTAGGTGTTGTGGTTTGGCCCTCCAGGACCTGACGGA 366
 341 GGTCCAGCGTACTCGGTAGGTGTTGTGGTTTGGCCCTCCAGGACCTGACGGA 282
 367 CACACGACATCATCAGTATGACGACCTTACAGGACCATCCAGGATTCATCCAG 426
 281 CCCACGACATCAGGATTTGGGATGAACCTCTGCGAGACCATCAAGTTACATTA 222
 427 TACGACCCCATATACGTGCCATCGTAGTGCCTCCCTAGGCGCATCAATACCCACATTTGGC 486
 221 TACGACCCCATATACGTGCCATTTAGTACCCCTCGGGGCAATTCATGACCCATGCTGGC 162

QY 487 CTCGATCGAGAGCTCGGGCACCGCCTATC-GGGTCGATCGGCCCAACAGCATGTATGGAC 545
 Db 161 CTCGATCGAGAGCTCGAGCACCGCCTATCGGGTCTGATCGGCCACACGGTGTATGGAC 102
 QY 546 AGTTGTTGGGTACTCTCATAGTACACCATTAAGTGAAGTCACAAAAGCCAGAGGGA 605
 Db 101 AGTTGTTGG--CGTACCTCGATAGTGGCAGCATAAAGTGAAGTCACAAAAGCCAGAGGAA 44
 QY 606 GAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGAAAT 647
 Db 43 GAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGAAAT 2

RESULT 10

EG130690/c
 LOCUS
 DEFINITION
 639 bp mRNA linear EST 31-JAN-2001
 EST463582 tomato crown gall Lycopersicon esculentum cDNA clone cTOB1A9 5' sequence similar to putative pathogenesis-related protein PR P23, mRNA sequence.

ACCESSION

EG130690
 EG130690.1 GI:12630878
 EST.

KEYWORDS

Lycopersicon esculentum (tomato)

ORGANISM

Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 639)

REFERENCE

van der Hoeven, R., Sun, H., Cho, J., Uterback, T., Hansen, C.,

AUTHORS

Renning, C. and Tanksley, S.

TITLE

Generation of ESTs from tomato crown gall tissue

JOURNAL

Unpublished (2001)

COMMENT

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES

Location/Qualifiers

1..639

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="cTOB1A9"

/tissue_type="crown gall"

/dev_stage="crown galls from full-grown plants (8 wks old)"

/lab_host="SOLR"

/clone_lib="tomato crown gall"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Four wk old greenhouse plants were stab inoculated on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr, Cornell U.). Galls were allowed to develop for another 4 wks, when gall tissue was frozen in liquid nitrogen."

ORIGIN

Query Match 28.3%; Score 451.6; DB 12; Length 639;
 Best Local Similarity 87.8%; Pred. No. 1e-83;
 Matches 516; Conservative 0; Mismatches 69; Indels 3; Gaps 2;
 49 ATCTTTGTTGAAAATAATTGGAAAGACGTAGGACCATGACCTTGGGTGCAACAAT 108
 587 ATCTTTGTTGAAAATAATTGGAAAGACGTAGGACCATGACCTTGTGTGCAACAAT 528
 QY 109 ATTGTTGTCTCCCAATGTGTACAGGATTTTACATCTCCGGTACTTTTAAAGCTGAC 168
 Db 527 ATTGTTGTCTCCGAACGTGTACAGGATTTTACATCTCCGGTACCTTAAGTGAAC 468
 QY 169 TAGGACATTCACCATTTATTTTGGCGTCATTTGAATTGTGTGGCATTTCCCTCCACTTG 228
 Db 467 CAGGACATTCACCATTTATATTAGCGGTACAATGAATTGCATGGCATTTCCCTCCACTAG 408
 QY 229 GATTAGTCGGGGGGAAGTCATCGGTATATTAAATCCATCAACTAAGAAATGTCCCGA 288

Db 407 GATTGGTGGGGCGAAAGTATTGGAATATTAATCCATCGACTAAAGAAATGCCAGA 348
 Qy 289 AATCTAAGTTGTTTGAACCTGGTCCAGGCTACTCGGCTAGGCTGTTTGGTGGTTTGCACC 348
 Db 347 AATCTAAGTTGTTTGAACCTGGTCCAGGCTACTCGGCTAGGCTGTTTGGTGGTTTGCACC 288
 Qy 349 ACCCGGTGCACTGCGAGCACACCAACAATCACCAAGTCATGCGACGAACTCTTACCAAGCAC 408
 Db 287 ACCCGGTGCACTGCGAGCACACCAACAATCACCAAGTCATGCGACGAACTCTTACCAAGCAC 228
 Qy 409 CACCGAAGTTACATCCAGTAGCGACCCCATATAGTCCATCGTAGTGCCCTAGGCGCAT 468
 Db 227 CATCAAGTTGCAATTCGTAGACCCCATATAGTCCATCTTAGTGCCCTCGGTGCAT 168
 Qy 469 CAATGACCCCATTTGGCCTCGATCGAGAGCTCGGGCACCGCCTA-TCGGGTGCAATGCCG 527
 Db 167 TGATGACCCCATTTGGCCTCGATCGAGAGCTCGACCACCGCCTATTGGGGTGCAGCGCG 108
 Qy 528 CCCAAACGATGTATGACAGTTGTTGGCGGTACTCTCGATAGTCACAGCATAGTGAAGT 587
 Db 107 CCCAGACGGGTATGACAGTTGTTGG-CCGATCTCGAAAGTGGCAGCATAGTGAAGT 50
 Qy 588 CACAAAAGCAGAGGAGGAGAAACCAAAAGAAAGATCTCAAGTAGCCCAT 635
 Db 49 CACAAAAGCAGAGGAGGAGAAACCAAAAGAAAGATCTCAAGTAGGCCAT 2

RESULT 11
 Bi922472/c
 LOCUS EST542376 tomato callus Lycopersicon esculentum cDNA clone
 DEFINITION cLEC77J15 5' end, mRNA sequence.
 ACCSSION Bi922472.1 GI:16219560
 VERSION EST.
 KEYWORDS Lycopersicon esculentum (tomato)
 SOURCE Lycopersicon esculentum
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 667)
 Alcalá, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A.,
 Tsai, J., Utterback, T., Van Aken, S., Renning, C.M., Fraser, C.M.,
 Martin, G.B., Tanksley, S.D. and Giovannoni, J.
 Generation of ESTs from tomato callus tissue (2001)
 Unpublished (2001)
 Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 This clone is available through the Clemson University Genomics
 Institute

Seq primer: T3.
 Location/Qualifiers
 1. .667
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cLEC77J15"
 /tissue_type="callus"
 /dev_stage="25-40 days old"
 /lab_host="XLI-Blue MRP"
 /clone_lib="tomato callus"
 /notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; supplier: Boyce Thompson Institute; sequencing: The
 Institute for Genomic Research; cLEC - Cotyledons; The
 seedlings 7-10 days post-germination were excised, cut at
 both ends and placed on MS medium with no selection. Mixed
 callus was harvested at 25 and 40 days and included
 undifferentiated masses. Tomato Callus EST Library"

FEATURES

source

ORIGIN

Query Match 28.1%; Score 449.6; DB 12; Length 667;
 Best Local Similarity 86.4%; Pred. No. 2.6e-83;
 Matches 520; Conservative 0; Mismatches 79; Indels 3; Gaps 2;
 Qy 47 GTATCTTTGTTGAAAAAATTGAAAAAGAGCTAGGACCAATCGACCTTGGGTGCAACA 106
 Db 601 GGCACATCTTGTGTTGAAAAATCTCGAAAAATCAGTAGTAGGCGCACATGGACCTTTGTGTGCAACA 542
 Qy 107 ATATTGTTGTTCTCCAAATGTGGTACAGGATTCTTACATCTCCGGGTACTTTAAGCTG 166
 Db 541 ATATTGTTGTTCTCCGAACGTGGTACAGGATTCTTACATCTCCGGGTACCTTAAGTGA 482
 Qy 167 ACTAGACATTCACCATTTATTTTGGCGTGCATTTGAATTGTGTGGCATTTCCCTCCACT 226
 Db 481 ACCAGACATTCACCATTTATATTAGCGTACAAATGAATTGCATGGCATTTCCCTCCACT 422
 Qy 227 TGGATTAGTGGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCCA 286
 Db 421 AGGATTGTGGGGCGAAAGTCATTGGAATATTAAATCCATCGACTAAAGAAATGTCCCA 362
 Qy 287 GAAATCTAAGTTGTTGAACTGGTCCAAAGGCGTACTCGGCTAGGCTGTTTGGTGGTTTGGC 346
 Db 361 GAAATCTAAGTTGTTGAACTGGTCCAAAGGCGTACTCGGCGAGGGTGTGTTGGTGGTTTGGC 302
 Qy 347 CCACCGGTGCACTGCAGGACACCAACACATCACAGTATGACGACGACCTTACCAGC 406
 Db 301 CCACCGGTGCACTGCAGGACACCAACACATCACAGTATGACGACGACCTTACCAGC 242
 Qy 407 ACCACCGAAGTTACATCCAGTACGACACCCCATATATACGTGCCATCGTAGTGCCTTAGGCGC 466
 Db 241 ACCATCAAGTTGCAATTTCGTACGACCCCATATATACGTGCCATCTTAGTGCCTTAGGCGC 182
 Qy 467 ATCAATGACCCACATTTGGCCTCGATCGAGACGTGCGGGACCGCCTA-TCGGGTGCAATGC 525
 Db 181 ATTGATGACCCATGTTTGGCCTCGATCAAGACGTGCGACCCGCTATTGGGGTGCAGCGC 122
 Qy 526 CGCCCAACGATGTATGGACAGTTGTTGGCGGTACCTCGATAGTGACAGATAAGTGA 585
 Db 121 CGCCAGACGGTGTATGGACAGTTGTTG--CGTACCTCGAAAGTGGCAGCATAGTGTAA 64
 Qy 586 GTCAAAAGCCAGAACGGAGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGTAA 645
 Db 63 GTCAAAAGCCAGAACGGAGAGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGTAA 4
 Qy 646 AT 647
 Db 3 CT 2

BF053678 622 bp mRNA linear EST 07-MAR-2003
 EST438908 potato leaves and petioles Solanum tuberosum cDNA clone
 C5TB36B20 5' sequence, mRNA sequence.
 BF053678
 BF053678.1 GI:10807574
 EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum

RESULT 12
 BF053678/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 622)
 van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
 Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R.,
 Renning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Generation of ESTs from potato leaves and petioles
 Unpublished (2000)
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/.

FEATURES

source
1..622
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cS7B36B20"
/tissue_type="leaves and petioles"
/dev_stages="8 weeks old plants"
/lab_host="SOLR"
/clone_lib="potato leaves and petioles"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Tissue was supplied by Dr. Fry (Cornell University).
Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."

ORIGIN

Query Match 28.1%; Score 449; DB 10; Length 622;
Best Local Similarity 86.9%; Pred. No. 3.5e-83;
Matches 517; Conservative 0; Mismatches 75; Indels 3; Gaps 2;
QY 46 GGTATCTTTTGAAGAAATGGAAAGACGTAGGACCAATGGACCTTGGGTGCAAC 105
Db 602 GGCATCTTTTGAAGAAATCGACCAATGAGTGGACCAATGGACCTTGGGTGCAAC 543
QY 106 AATATGTTGCTCCCAATGTTGACAGGATTTTACATCTCCGGTACTTTAGCT 165
Db 542 AATATGTTGCTCCCAATGTTGACAGGATTTTACATCTCCGGTACTTTAGCT 483
QY 166 GACTAGGACATTCACCATTTATTTGCGGTGATTTGAATTTGTCGATTTCCCTCCAC 225
Db 482 GACCAAGGATTCACCATTTATTTGCGGTGATTTGAATTTGTCGATTTCCCTCCAC 423
QY 226 TTGATTTAGTCCGGGGGAAAGTCTATCGGTATTTAAATTCATCACTAAAGAAATGCC 285
Db 422 TAGGATTTGTCGGGGGAAAGTCTATCGGTATTTAAATTCATCACTAAAGAAATGCC 363
QY 286 AGAATCTTAAGTTTGAATCTGTCAGGCGTACTCGGTAGGCTTTGGTGGTTTGC 345
Db 362 AGAATCTTAAGTTTGAATCTGTCAGGCGTACTCGGTAGGCTTTGGTGGTTTGC 303
QY 346 CCCACCGGTGCTAGGACACCAACCAATCAACAGTCAAGCAGCACTCTACAG 405
Db 302 CCCACCGGTGCTAGGACACCAACCAATCAACAGTCTAGCAAGCACTCTACAG 243
QY 406 CACCACCAAGTTACATCCAGTACGCCATATACGTGCGATCTAGTCCCTAGCG 465
Db 242 CACCATCAAGTTGCAATTTAGTACGCCATATACGTGCGATCTAGTCCCTAGCG 183
QY 466 CATCAATGACCCACATTTGGCTCGATCGAGACCTCGGACCCCTATC-GGTCGATG 524
Db 182 CATTTAGTACCCCAAGTTGACCTCGATCGAGACCTCGGACCCCTATCGGGTGTATG 123
QY 525 CCGGCCCAACGATGTATGACAGTTTGGCGGTACCTCGATGTAGCAGCATTAAGTAA 584
Db 122 CCGGCCCAACGATGTATGACAGTTTGGCGGTACCTCGATGTAGCAGCATTAAGTAA 65
QY 585 AGTCACAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTT 639
Db 64 AGTCACAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTT 10

RESULT 13

AW031249/c

LOCUS

DEFINITION EST274624 tomato callus, TAMU lycopersicon esculentum cDNA clone
cLEC34F24 similar to osmotin-like protein TPM-1 precursor (PR F23),

ACCESSION

AW031249

VERSION AW031249.1 GI:5889926

KEYWORDS

EST.

SOURCE

Lycopersicon esculentum (tomato)

ORGANISM

Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 585)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Kolt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S.,
Romling,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
Giovannoni,J.

Generation of ESTs from tomato callus tissue

Unpublished (1999)

CONTACT

CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: http://www.genome.clemson.edu/orders/index.html

5 prime sequence.

FEATURES

Location/Qualifiers

1..585
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
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/clone="cLEC34F24"
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/dev_stages="25-40 days old"
/lab_host="XL1-Blue MRP"
/clone_lib="tomato callus, TAMU"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"

ORIGIN

Query Match 28.0%; Score 447.2; DB 9; Length 585;
Best Local Similarity 87.5%; Pred. No. 8.5e-83;
Matches 511; Conservative 0; Mismatches 70; Indels 3; Gaps 2;
QY 67 TGAAGAAGACGTAGGACCAATGGACCTTGGGTGCAACAATATTTGTCCTCCAAATG 126
Db 583 TGCACAAATCAGTAGGNCACATGGACCTTGTGTGCAACAATATTTGTCCTCCGAAAG 524
QY 127 TGTACAAGGATTTTACATCTCCGGGTACTTTAAGCTGACTAGGACATTCACCAATTTA 186
Db 523 TGTACAAGGATTTTACATCTCCGGGTACTCCNAAAGTGAACACGACATTCACCAATTTA 464
QY 187 TATTTGCCGTGCAATGAATTTGTGTGCAATTTCCCTCCACTTGGATTTAGTCGGGGGAAAG 246
Db 463 TATTAGCCGTACAATGAATTTGATGTCATTTCCCTCCACTAGGATTTGTCGGGGGAAAG 404
QY 247 TCATCGGTATTTAAATCCATCACTAAAGAAATGTCCAGAAATCTAGATTTGTTGAATCT 306
Db 403 TCATTCGAATATTTAAATCCATCACTAAAGAAATGTCCAGAAATCTAGATTTGTTGAATCT 344
QY 307 GGTCCAAGCGTACTCGGCTAGGGTGTTTGGTGGTTTGGCCACCCCGGTGCTACGAGA 366
Db 343 GGTCCAAGCGTACTCGGCGAGGGTGTTTGGTGGTTTGGCCACCCCGGTGCTACGAGA 284
QY 367 CACCACCAATCAACGATTCAGCAACCTCTACGACCACTCCAGCAACCTGATTCACAG 426
Db 283 CCCCACCAATCAACGATTCAGCAACCTCTCTACGACCACTCCAGCAACCTGATTCACAG 224
QY 427 TAGCAGCCCATATACGTGTCATCGTAGTCCCTCCTAGGCGCATCAATGACCCACATTTGGC 486
Db 223 TAGCAGCCCATATACGTGTCATCGTAGTCCCTCCTCCTAGGCGCATCAATGATGCCATTTGGC 164

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QY 487 CTCGATCGAGACGTCGGGCGCCGCTA-TCGGGTCGATGCGGCCCAACCGATGTATGGAC 545
Db 163 CTCGATCAAGACGTCGACCGCCTATTGGGTCGACGCGCCGACGCGTGTATGGAC 104
QY 546 AGTTGTTGGCGGTACCTCGATAGTCAGCATAGTAAAGTCACAAAAGCCAGAGGGA 605
Db 103 AGTTGTTG--CGTACCTCGAAGTGGCGCATAGTGTAAAGTCACAAAAGCCAGAGGGA 46
QY 606 GAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGAAATTT 649
Db 45 GAAACCAAAAGAGATCTCAAGTAGGCCATGTTTGTGGAACAT 2

RESULT 14
AW032915/c
LOCUS
DEFINITION EST276474 tomato callus, TAMU Lycopersicon esculentum cDNA clone
ACCESSION AW032915
VERSION AW032915.1 GI:5891671
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 583)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T.,
Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S.,
Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
Giovannoni, J.
Generation of ESTs from tomato callus tissue
Contact: CUGI
Unpublished (1999)
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.

FEATURES
Location/Qualifiers
source
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/mol_type="mRNA"
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/db_xref="taxon:4081"
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/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XJ1-Blue MRF"
/clone_lib="tomato callus, TAMU"
/notes="Supplier: pBlueScript SK(-); Site 1: EcoRI; Site 2:
XhoI; Supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"

ORIGIN
Query Match 27.6%; Score 440.8; DB 9; Length 583;
Best Local Similarity 87.1%; Pred. No. 1.8e-81;
Matches 507; Conservative 0; Mismatches 72; Indels 3; Gaps 2;

QY 67 TGGAAAGACGTAGGACCAATGGACCTTGGGTGCAATATTTGTTCTCCAAATG 126
Db 581 TCGACAATCAGTAGGGCCCATGGACCTTGTGTGCAACAATATTTGTTCTCCAAACG 522
QY 127 TGGTACAGGATTTTACATCTCCGGGTACTTTAAGCTGACATGACATTCACCATTTA 186
Db 521 TGGTACAGGATTTGTTACATCTCCGGGTACTGTTAGTGACACGACATTCACCATTTA 462
QY 187 TATTGCGGTGCAATGTAATTTGTGTGGCATTTCCCTCCACTTGGATTAGTCGGGGCGAAAG 246
Db 461 TATTAGCCGTACAATGAATTTGCAATGGCATTTCCCTCCACTTAGGATTGGTTCGGGGCGAAAG 402

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QY 247 TCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCAGAAATCTAAGTTGTGAAC 306
Db 401 TCATTGGAATATTAAATCCATCGACTAAAGAAATGTCCAGAAATCTAAGTTGTGAAC 342
QY 307 GGTCCAAGCGCTACTCGGTAGGCTGTTTGGTGTGTTTGGCCACCCGTCGACATGACGA 366
Db 341 GGTCCAAGCGCTACTCGGTAGGCTGTTTGGTGTGTTTGGCCACCCGTCGACATGACGA 282
QY 367 CACCACCAATCAATCAGTCTATGACGAACTCTACAGCAGCACCAGGATACATCCAG 426
Db 281 CCCCACCAATCAATCAGTCTGACATGAACCTCTACAGCAGCACCATCAAGTTGCAATTC 222
QY 427 TAGGACCCCATATAGTGTCCATCTAGTGCCTCTAGGCGCATCAATGACCCACATTTGGC 486
Db 221 TAGGACCCCATATAGTGTCCATCTAGTGCCTCTAGGCGCATCAATGACCCATGTTTGGC 162
QY 487 CTCGATCGAGACGTCGGGCGCCGCTA-TCGGGTCGATGCGGCCCAACCGATGTATGGAC 545
Db 161 CTCGATCGAGACGTCGACCCGCTATTGGGTCGACGCGCCCGCAGCGGTGTATGGAC 102
QY 546 AGTTGTTGGCGGTACCTCGATAGTCAGCATAGTGAAGTCAAAAAGCCAGAGGGA 605
Db 101 AGTTGTTG--CGTACCTCGAAGTGGCGCATAGTGTAAAGTCACAAAAGCCAGAGGGA 44
QY 606 GAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGAAAT 647
Db 43 GAAACCAAAAGAGATCTCAAGTAGGCCATGTTTGTGGAAC 2

CK273930 923 bp mRNA linear EST 12-DEC-2003
EST720008 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POADE25 5' end, mRNA sequence.

ACCESSION CK273930
VERSION CK273930.1 GI:39830908
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 923)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST720009
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
Location/Qualifiers
1..923
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POADE25"
/tissue_type="abiotic stress treated leaf and root tissue"
/clone_lib="potato abiotic stress cDNA library"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
Supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then

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were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Query Match	27.5%	Score 439.2;	DB 14;	Length 923;
Best Local Similarity	85.6%	Pred. No. 3.5e-81;		
Matches 512;	Conservative 0;	Mismatches 83;	Indels 3;	Gaps 2;
Qy	46	GGTATCTTTGTTGAAAGAAATTTGAAAGAACGTAGGACACATGGACCTTGGGTGCAAC	105	
Db	601	GGCATCTTTTGGAAAATTTGGACAACTCTGTAGACCACTGGACCTTGGGTGAGC	542	
Qy	106	AATATTGTTGTCCTCCAAATGTGTACAAGATTGTACATCTCCCGGGTACTTTAAGCT	165	
Db	541	AATATTGTTGTCCTCCGAATGTGTACAAGATTGTACATCTCCCGGGTACTTTAAGG	482	
Qy	166	GACTAGGACATCCACATTTATATTGCGGTGCAATTGAAATGTGTGGCATTTCCCTCCAC	225	
Db	481	CGCAGGACATCCACATTTATATTGCGGTGCAATGAATGCAATGCAATTTCCAGCAC	422	
Qy	226	TTGGATTAGTCGGGGCGAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCC	285	
Db	421	TAGGTTTGGTTGGGCAAGTCATTGGAAATTTGAATCCGTCAACTAAAGAAATATCCC	362	
Qy	286	AGAAATCTAAGTTGTGAACTGGTCCAAAGCGTACTCGGCTAGGTGTTTGGTGGTTGC	345	
Db	361	AGAAATCTAGTTGTGCTAACTGATCCAAAGGCATATTAGCCAAAGTGTGTTGGGGGCTGC	302	
Qy	346	CCCACCGGTGCACCTGCAGGACACCCACCAATCACCAGTCATGCACGAACCTCTACCAG	405	
Db	301	CCCACCGGTACACTGCAGACTCCACCAATCACCAGTCATGCACGAACCTCTGCTG	242	
Qy	406	CACCACGAAGTTACATCCAGTAGACCCCATATACGTGCCATCGTAGTGCCCTAGGCG	465	
Db	241	CAGCATTGAAGTTACACCACTAGACCCCATATACGTGCCATCTTAGTTCCTCCCTTGAG	182	
Qy	466	CATCAATGACCCACATTTGGCTCGATCGAGCGTCGGGACCCGCTATC-GGGTCGATG	524	
Db	181	CATTGATGACCCATGTTTGGGCTTTATTGAGACGTGACACCCGCTATCGGGGTGATG	122	
Qy	525	CCGCCAAACGATGTATGACAGTTGTTGGCGGTACCTCGATAGTAGCAGCATAAAGTAA	584	
Db	121	CTGCCCAACAGGTGTATGACAGTTGTTG--CGTACCTCGATAGTGGCAGCATAAAGTAA	64	
Qy	585	AGTCAAAAGCCGAGAGGGAGAACCAAAAGAGATCTCAAGTAGCCCATGTTGTT	642	
Db	63	AGTCACAAAGCAGAGGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTAAAT	6	

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 07:30:51 ; Search time 679.862 Seconds
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11157.588 Million cell updates/sec

Title: US-10-051-307-3

Perfect score: 1546

Sequence: 1 atcttggttgaaaaattg.....tggtgaagtgtgtgtttc 1546

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1545	99.9	1546	14	US-10-051-307-3
2	1362.4	88.1	1595	14	US-10-051-307-1
3	1334.4	86.3	1598	14	US-10-051-307-2
C 4	291.2	18.8	510	16	US-10-341-961A-371
C 5	207.2	13.4	735	9	US-09-938-842A-2118
C 6	207.2	13.4	735	11	US-09-938-842A-2118
C 7	207.2	13.4	950	9	US-09-770-445-334
C 8	182.4	11.8	809	13	US-10-424-599-103619
C 9	180.6	11.7	875	17	US-10-636-396-4
C 10	180.6	11.7	875	17	US-10-636-026-4
C 11	171.6	11.1	1566	13	US-10-424-599-36321
C 12	155.8	10.1	717	15	US-10-259-165-389
C 13	155.8	10.1	720	15	US-10-259-165-41
C 14	153.6	9.9	1006	17	US-10-437-963-86607

C 15	145.4	9.4	1173	13	US-10-424-599-7736
C 16	142.6	9.2	696	15	US-10-259-165-353
C 17	142.6	9.2	699	15	US-10-259-165-109
C 18	142.6	9.2	1052	17	US-10-437-963-89569
C 19	140.6	9.1	1020	15	US-10-259-165-571
C 20	140.6	9.1	1020	16	US-10-260-238-3136
C 21	135.6	8.8	805	16	US-10-260-238-4061
C 22	135.6	8.8	879	13	US-10-260-238-49
C 23	135.4	8.8	901	13	US-10-424-599-7737
C 24	135.2	8.7	911	13	US-10-425-114-27634
C 25	133.8	8.7	922	16	US-10-260-238-4067
C 26	115.4	7.5	343	9	US-09-770-791-806
C 27	112.8	7.3	1950	17	US-10-437-963-59877
C 28	109.4	7.1	3630	17	US-10-437-963-16245
C 29	104.4	6.8	808	9	US-09-966-881-46
C 30	104	6.7	1928	13	US-10-425-114-24457
C 31	102.4	6.6	869	17	US-10-437-963-15621
C 32	100.4	6.5	633	15	US-10-259-165-532
C 33	100.4	6.5	633	16	US-10-260-238-5182
C 34	94	6.1	621	15	US-10-175-389-1
C 35	92.8	6.0	621	15	US-10-175-389-9
C 36	91.8	5.9	730	13	US-10-425-114-25389
C 37	91.8	5.9	826	13	US-10-425-114-23076
C 38	91.6	5.9	973	17	US-10-437-963-16928
C 39	88.8	5.7	728	16	US-10-260-238-3135
C 40	86	5.6	730	13	US-10-425-114-27495
C 41	83.4	5.4	904	13	US-10-425-114-28239
C 42	82.6	5.3	891	17	US-10-437-963-49328
C 43	81	5.2	721	13	US-10-425-114-2055
C 44	81	5.2	753	13	US-10-425-114-23100
C 45	81	5.2	807	13	US-10-425-114-15687

ALIGNMENTS

RESULT 1

US-10-051-307-3

; Sequence 3, Application US/10051307
; Publication No. US20020170095A1
; GENERAL INFORMATION:
; APPLICANT: DAI, ZIYU
; APPLICANT: SHI, LIFANG
; APPLICANT: HOOKER, BRIAN S.
; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
; FILE REFERENCE: 059440/0141
; CURRENT APPLICATION NUMBER: US/10/051,307
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,224
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1546
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1248)
; OTHER INFORMATION: a, t, c or g
US-10-051-307-3

Query Match 99.9%; Score 1545; DB 14; Length 1546;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATCTTTGTTGAAAAATTGGAAAGAACCTAGACACATGGACCTTGGGTGCAACAT	60
Db	1	ATCTTTGTTGAAAAATTGGAAAGAACCTAGACACATGGACCTTGGGTGCAACAT	60
Qy	61	ATTGTTGTTCTCCAAATGTGTACAGGATTGTACATCTCCGGGTACTTTAAGTGAC	120
Db	61	ATTGTTGTTCTCCAAATGTGTACAGGATTGTACATCTCCGGGTACTTTAAGTGAC	120

QY	121	TAGGACATTACACATTTATTTGTCGGTGCATTTGAAATTGCGTGGCATTTCCCTCCACTTG	180
DB	121	TAGGACATTACACATTTATTTGTCGGTGCATTTGAAATTGCGTGGCATTTCCCTCCACTTG	180
QY	181	GATTAGTCGGGGCGAAAGTCATCGGTAATTAAATCCATCAACTAAAGAAATGTCGCCAGA	240
DB	181	GATTAGTCGGGGCGAAAGTCATCGGTAATTAAATCCATCAACTAAAGAAATGTCGCCAGA	240
QY	241	AATCTAAGTTGTTGAACCTGGTCCGAGGCGTACTCGGCTAGGTTGGGTTTACCC	300
DB	241	AATCTAAGTTGTTGAACCTGGTCCGAGGCGTACTCGGCTAGGTTGGGTTTACCC	300
QY	301	ACCGGTGCACCTGCAGGACACACCAAAATCACCAGTCATGCACGAACCTCTACAGGAC	360
DB	301	ACCGGTGCACCTGCAGGACACACCAAAATCACCAGTCATGCACGAACCTCTACAGGAC	360
QY	361	CATCGAAGTTACATCGAGTAGACCCCATATACGTGCCATCGTAGTGCCTTAGCGCAT	420
DB	361	CATCGAAGTTACATCGAGTAGACCCCATATACGTGCCATCGTAGTGCCTTAGCGCAT	420
QY	421	CAATGACCCACCGTTTGGCTCGATCGAGACGTGGCCACCGCTATCGGGTTCGATCGT	480
DB	421	CAATGACCCACCGTTTGGCTCGATCGAGACGTGGCCACCGCTATCGGGTTCGATCGT	480
QY	481	CCGACGCGTGTATGGAACAGTTTGGTCTTATATATAGGGATATGGCGCTTTTGGCACTA	540
DB	481	CCGACGCGTGTATGGAACAGTTTGGTCTTATATATAGGGATATGGCGCTTTTGGCACTA	540
QY	541	CAAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAATTT	600
DB	541	CAAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAATTT	600
QY	601	ATATGTGACAAATTAATTTTGGTACTTATATATAGGGATATGGCGCTTTTGGCACTA	660
DB	601	ATATGTGACAAATTAATTTTGGTACTTATATATAGGGATATGGCGCTTTTGGCACTA	660
QY	661	TGGATTAATACTGATATATAACAATATCATATCTTTGACTAATTAATAACAATAATAT	720
DB	661	TGGATTAATACTGATATATAACAATATCATATCTTTGACTAATTAATAACAATAATAT	720
QY	721	TACAAATGATTTGGTAAACGTTGAGGTGGCAAAATGTATAAGAGCCGCTAAATAATAA	780
DB	721	TACAAATGATTTGGTAAACGTTGAGGTGGCAAAATGTATAAGAGCCGCTAAATAATAA	780
QY	781	TTATTTTATGAATATAGNACTATAGTTACAGTGAACCTTTATTTGTTGATTAACCTTGGACAT	840
DB	781	TTATTTTATGAATATAGNACTATAGTTACAGTGAACCTTTATTTGTTGATTAACCTTGGACAT	840
QY	841	ATAAATCTGTATCGTGACGGAACTTTTCTTAAACCTAAATATAAAAGGAGCTATTTT	900
DB	841	ATAAATCTGTATCGTGACGGAACTTTTCTTAAACCTAAATATAAAAGGAGCTATTTT	900
QY	901	AATATTTTTCGTGGCCAAAGTTTCTTGCATATCTTATCTATGCCCATTTTTACTTTTATCG	960
DB	901	AATATTTTTCGTGGCCAAAGTTTCTTGCATATCTTATCTATGCCCATTTTTACTTTTATCG	960
QY	961	TTCTAGCCTCTAGCTACGGTTTGAACATAAAAAATCATAAAAATTCGAAAGTAAAAAT	1020
DB	961	TTCTAGCCTCTAGCTACGGTTTGAACATAAAAAATCATAAAAATTCGAAAGTAAAAAT	1020
QY	1021	AGTTTCTTTCATATATCTCGTATGGACATTTGTTTGTAGATCAATGTGAATATACAAATC	1080
DB	1021	AGTTTCTTTCATATATCTCGTATGGACATTTGTTTGTAGATCAATGTGAATATACAAATC	1080
QY	1081	ATTCCTGATTTTAAATCATAACTATTTCTGCATGATGGGAACTGCTATGGTCAATTCGTGAC	1140
DB	1081	ATTCCTGATTTTAAATCATAACTATTTCTGCATGATGGGAACTGCTATGGTCAATTCGTGAC	1140
QY	1141	AAGTGTGTTGATTTATCTAAGCTGGAATGGAGTCACAACTTTTAGTGCATAATCTTAT	1200
DB	1141	AAGTGTGTTGATTTATCTAAGCTGGAATGGAGTCACAACTTTTAGTGCATAATCTTAT	1200

```

RESULT 2
US-10-051-307-1
; Sequence 1, Application US/10051307
; Publication No. US20020170095A1
; GENERAL INFORMATION:
; APPLICANT: DAI, ZIYU
; APPLICANT: SHI, LIFANG
; APPLICANT: HOOKER, BRIAN S.
; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
; FILE OF INVENTION: 059440/0141
; CURRENT APPLICATION NUMBER: US/10/051,307
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,224
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1.
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-051-307-1

```

Query Match	88.1%;	Score 1362.4;	DB 14;	Length 1595;
Best Local Similarity	94.1%;	Pred. No. 3.5e-289;		
Matches 1460;	Conservative 0;	Mismatches 82;	Indels 9;	Gaps 4;
Qy	1	ATCTTTGTTTGA	AAATTCG	GAARAAGAACGTAGGACACATGACCTTGGTGCAACAAT 60
Db	49	ATCTTTGTTTGA	AAATTCG	GAARAAGAACGTAGGACACATGACCTTGGTGCAACAAT 108
Qy	61	ATTGTTGTCTC	CAAAATG	TGGTCAAGGATTGTATCATCTCCGGGTACTTTTAAGCTGCAC 120
Db	109	ATTGTTGTCTC	CAAAATG	TGGTCAAGGATTGTATCATCTCCGGGTACTTTTAAGTTGAC 168
Qy	121	TAGGACATTC	CACCATTTAT	TTCGCGTGCAATTGAATTCGCTGGCATTTCCCTCCACTTG 180
Db	169	CAGGGCATTC	CACCATTTAT	TTCGCGTGCAATTGAATTCGCTGGCATTTCCCTCCACTTG 228
Qy	181	GATTAGTCGG	GGGCGAAGT	CATCGGTATATTAATCCATCAACTAAAGAAATGTC
Db	229	GATTAGTCGG	GGGCGAAGT	CATCGGTATATTAATCCATCAACTAAAGAAATGTC
Qy	241	AATCTAAGTT	GTGTGA	CTGGTCCGAGCGGTACTCGGCTAGGGTGTTTGGCGGTTTACCCC 300
Db	289	AATCTAAGTT	GTGTGA	CTGGTCCGAGCGGTACTCGGCTAGGGTGTTTGGTGTGTTGCCCC 348
Qy	301	ACCCGGTGC	ACTG	CAGGACACCAACAATCACTCATGTCACGAACCTCTTACCAGCAC 360

Db 349 ACCGGTGCATCGAGGACACCAACATACAGTCATGACGAACTCTACCAGCAC 408
 Qy 361 CATCGAAGTTACATCCAGTAGAGCCCATATACGTCGATCGTAGTGCCTTACGGCGCAT 420
 Db 409 CATCGAAGTTACATCCAGTAGAGCCCATATACGTCGATCGTAGTGCCTTACGGCGCAT 468
 Qy 421 CAATGACCCAGTTTGGCTCGATCGAGACGTCGGCCACCGCTATCGGGGTGCGATGCTG 480
 Db 469 CAATGACCCAGTTTGGCTCGATCGAGACGTCGGCCACCGCTTTCGGGGTGCATGCCG 527
 Qy 481 CCCAGACGGTGTATGAGCAGTTGTGCGTACCTCGATAGTGGCAGCAGTAAGTGAAGTCA 540
 Db 528 CCCAAGCATGTATGAGCAGTTGTGCGTACCTCGATAGTGGCAGCAGTAAGTGAAGTCA 587
 Qy 541 CAAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 Db 588 CAAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 647
 Qy 601 ATATGTGGACAAATTAATTTTGGTACTTATATATAGGATATGGCGGCTTTTGGCACTA 660
 Db 648 ATATGTGGACAAATTAATTTTGGTACTTATATATAGGATATGGCGGCTTTTGGCACTA 707
 Qy 661 TGGATATTAATCGTATTAATAACAATATCATATCTTGAATTAATTAATAACAATATAT 720
 Db 708 CGGATATTAATCGTATTAATAACAATATCATATCTTGAATTAATTAATAACAATATAT 767
 Qy 721 TACAATATGATTTCGTAACCGTTGAGGTGGCAAAATGTATAAGAGCGCCCTAATAATTA 780
 Db 768 TACAATATGATTTCGTAACCGTTGAGGTGGCAAAATGTATAAGAGCGCCCTAATAATTA 827
 Qy 781 TTATTTATGAATATAGACTATAGTCAAGTGAACCTTTATTTGGTGAATTAATTTGGACAT 840
 Db 828 TTATTTATGAATATAGACTATAGTCAAGTGAACCTTTATTTGGTGAATTAATTTGGACAT 887
 Qy 841 ATAAACTCTGATCGTGAAGCACTTTTCTTAAACTAAATATTAATAAGCAGCTATTTT 900
 Db 888 ATAAACTCTGATCGTGAAGCACTTTTCTTAAACTAAATATTAATAAGCAGCTATTTT 947
 Qy 901 AATATTTTTCGTGCCAAAGTTTCTGATCACTTATCTATGCCCATTTTACTTTTATCG 960
 Db 948 CAGATTTTTCGTGCCAAAGTTTCTGATCACTTATCTATGCCCATTTTACTTTTATCG 1007
 Qy 961 TTCTAGCCCTTAGTACGCGTTTGAACATATAAAATCATAAAATTAAGAGTAAATTT 1020
 Db 1008 TTCTAGCCCTTAGTACGCGTTTGAACATATAAAATCATAAAATTAAGAGTAAATTT 1067
 Qy 1021 AG---TTT---TTTTCATATTAATCGTATGATGATCTTGTAGATCAATGTGAATATACAA 1077
 Db 1068 AGTTT---TTTTCATATTAATCGTATGATGATCTTGTAGATCAATGTGAATATACAA 1127
 Qy 1078 ATCATCTGATTTTAAATATCAATATCTTGTGATGATGGAACGTCATGGTATTCGT 1137
 Db 1128 ACCATCTGATTTTAAATATCAACCAATCTGCAAGGGGAAGTCTAT--GTGATCCGT 1184
 Qy 1138 GACAGTCTGATTTTATTTTAAAGTCTGATGATGATGATGATGATGATGATGATGATGAT 1197
 Db 1185 GACAGTCTGATTTTATTTTAAAGTCTGATGATGATGATGATGATGATGATGATGATGAT 1244
 Qy 1198 ATTAAGAGACCCCTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1255
 Db 1245 ATTAAGAGACCCCTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1304
 Qy 1256 TATTTTATGATCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1315
 Db 1305 TATTTTATGATCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1364
 Qy 1316 CGACAGTCAATCAAGCTTATCGTCAATCCACATTCCTTAAAGTGTAGTATGCTGCTTTT 1375
 Db 1365 CGACAGTCAATCAAGCTTATCGTCAATCCACATTAAGTGTAGTATGCTGCTTTT 1424
 Qy 1376 AGAGAAAACAGTGGATCATGATTAATTTAGTTTCCCTTATCTCTAATAATATCTATAT 1435
 Db 1425 AGAGAAAACAGTGGATCATGATTAATTTAGTTTAAATATCTCTCTAATAATATCTATAT 1484

Qy 1436 ATACCTCTAAACTAAATGATCTAAACAAACAAATATAAACTTAGATTTCTTTAAGAAA 1495
 Db 1485 ATACCTCTAAACTAAATGATCTAAACAAACAAATATAAACTTAGATTTCTTTAAGAAA 1544
 Qy 1496 TTGCAGAAATTAATGAGGCAAAATTAAGTCTATGTTGAAGTTGGTTGCTTTC 1546
 Db 1545 TTGCAGAAATTAATGAGGCAAAATTAAGTCTATGTTGAAGTTGGTTGCTTTC 1595

RESULT 3

US-10-051-307-2
 ; Sequence 2, Application US/10051307
 ; Publication No. US20020170095A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DAI, ZIYU
 ; APPLICANT: SHI, LIPANG
 ; APPLICANT: HOOKER, BRIAN S.
 ; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
 ; FILE REFERENCE: 059440/0141
 ; CURRENT APPLICATION NUMBER: US/10/051,307
 ; CURRENT FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: 60/263,224
 ; PRIOR FILING DATE: 2001-01-23
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 1598
 ; TYPE: DNA
 ; ORGANISM: Solanum tuberosum
 US-10-051-307-2

Query Match 86.3%; Score 1334.4; DB 14; Length 1598;
 Best Local Similarity 93.8%; Pred. No. 5.1e-283;
 Matches 1456; Conservative 0; Mismatches 87; Indels 10; Gaps 6;

Qy 1 ATCTTTGTTTGAAGAAATTTGAAAGACCTAGGACCAATGACATCGACTTGGGTGCAACAAT 60
 Db 49 ATCTTTGTTTGAAGAAATTTGAAAGACCTAGGACCAATGACATCGACTTGGGTGCAACAAT 108
 Qy 61 ATTGTTGTCCTCCAAATGTTGTAAGAGATTTACATCCTCCGGGTACTTTAAGCTGAC 120
 Db 109 ATTGTTGTCCTCCAAATGTTGTAAGAGATTTACATCCTCCGGGTACTTTAAGCTGAC 168
 Qy 121 TAGGACATTCACCATTTATTTGCGTGCATTTGATTCGGTGGCATTTCCCTCCACTTG 180
 Db 169 TAGGACATTCACCATTTATTTTGGCGTCAATGATTTGTTGGGCAATTTCCCTCCACTTG 228
 Qy 181 GATTAGTCCGGGCGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAAATGTCCAG 240
 Db 229 GATTAGTCCGGGCGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAAATGTCCAG 288
 Qy 241 AATCTAAGTTTGAATCTGTCGGAGCGTACTCGGCTAGGTGTTTGGGGTTTACCCC 300
 Db 289 AATCTAAGTTTGAATCTGTCGGAGCGTACTCGGCTAGGTGTTTGGGGTTTACCCC 348
 Qy 301 ACCGGTGCATCTCAGGACACCAACCAATCACCAGTCAATGACCAACCTTACACGACAC 360
 Db 349 ACCGGTGCATCTCAGGACACCAACCAATCACCAGTCAATGACCAACCTTACACGACAC 408
 Qy 361 CATCGAAGTTTACATCCAGTACGACCCCATATACGTGCCATCGTGTGCGCCCTAGGGCGCAT 420
 Db 409 CACCGAAGTTTACATCCAGTACGACCCCATATACGTGCCATCGTGTGCGCCCTAGGGCGCAT 468
 Qy 421 CAATGACCCACGTTTGGCTCGATCGAGAGTCCGACCGCTATCGGGGTGCGATGCTG 480
 Db 469 CAATGACCCACATTTGGCTCGATCGAGAGTCCGACCGCTATCGGGGTGCGATGCTG 527
 Qy 481 CCAGAGCGTGTATGACAGTGTGTTG--CGTACCTCGATGTGGCAGCATTAAGTGAAGT 538
 Db 528 CCAGAGCGTGTATGACAGTGTGTTGCGCGTACCTCGATGTGGCAGCATTAAGTGAAGT 587
 Qy 539 CACAAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 598

Db 588 CACAAAGCGAGAGGAGAACCAAAAGAGATCTCAAGTAGCCCATGTTGTGAAAT 647
QY 599 TTATATGTGGCAAAATATTTTGTACTTTATATATAGGATATGGCGGCTTTTGGCAC 658
Db 648 TTATATGTGGCAAAATATTTTGTACTTTATATATAGGATATGGCGGCTTTTGGCAC 707
QY 659 TATGATATTAATCGTATATATACATATACATCTTGTACTAATATATAACAATAAT 718
Db 708 TACGGAATTAATCGTATATATACATATACATCTTGTACTAATATATAACAATAAT 767
QY 719 ATTACAATATGATTGGTAAACGTTGAGTGGCCAAATGTATAAGAGCGGCTTAATAAT 778
Db 768 ATTACAATATGATTGGTAAACGTTGAGTGGCCAAATGTATAAGAGCGGCTTAATAAT 827
QY 779 AATTATTTTATGAATATAGACTATAGTTTCAAGTGAATTTATTTGGTATATCTGGAC 838
Db 828 AATTATTTTATGAATATAGCTATAGTTTCAAGTGAATTTATTTGGTATATCTGGAC 887
QY 839 ATATAAACTCTGTATCGTGACGGAACTTTTCTTAAACCTAAATATATAAAGCAGCTATT 898
Db 888 ATATAAACTCTGTATCGTGACGGAACTTTTCTTAAACCTAAATATATAAAGCAGCTATT 947
QY 899 TTAATATTTTCTGGGCGCAAGTTCTTGCACTATCTATGCCCCATTTTACTTTTAT 958
Db 948 TTAATATTTTCTGGGCGCAAGTTCTTGCACTATCTATGCCCCATTTTACTTTTAT 1007
QY 959 CGTTCTAGCCCTTCAGTGTACGCTTTTGAACATATAAATCATATAAATTTGAAGTAAATA 1018
Db 1008 CGTTCTAGCCCTTCAGTGTACGCTTTTGAACATATAAATCATATAAATTTGAAGTAAATA 1067
QY 1019 TTAG---TTTTTTTTTCAATTAATCTGATGATCAATTTGTTAGATCAATGTGAATATAC 1075
Db 1068 TTAGTTTTTTTTTCAATTAATCTGATGATCAATTTGTTAGATCAATGTGAATATAC 1127
QY 1076 AAATCATCTGATTTTAAATCATACATCTTCTGATGATGGAAAGCTCATGGTGAATC 1135
Db 1128 AAACCATCTGATTTTAAATCATACATCTTCTGATGATGGAAAGCTCAT--GTGATTC 1186
QY 1136 GTGCAAGTGTGATTTATTTTAAAGTCTGATGATGATGATGATGATGATGATGATGATGAT 1195
Db 1187 GTGCAAGTGTGATTTATTTTAAAGTCTGATGATGATGATGATGATGATGATGATGATGAT 1245
QY 1196 CTATTAAGAAACCCCTATTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1253
Db 1246 CTATTAAGAAACCCCTATTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1305
QY 1254 TTTATTTTACGATCGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1313
Db 1306 TTTATTTTACGATCGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1365
QY 1314 ATGCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1373
Db 1366 ATGCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1425
QY 1374 TTAGAGAAACAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1433
Db 1426 TTAGAGAAACAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1485
QY 1434 ATATACCTCTAAACCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1493
Db 1486 CTATCCCTCTTAAACCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1545
QY 1494 AATTGAGATTTAAATGGAGGCAAAATAGTCTATGATGATGATGATGATGATGATGATGATGAT 1546
Db 1546 AATTGAGATTTAAATGGAGGCAAAATAGTCTATGATGATGATGATGATGATGATGATGATGAT 1598

RESULT 4

US-10-341-961A-371/c

; Sequence 371, Application US/10341961A

; Publication No. US20040006781A

; GENERAL INFORMATION:

; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
; APPLICANT: Curagen Corporation
; APPLICANT: Crasta, Oswald
; APPLICANT: Swirsky, Peter
; APPLICANT: Mysore, Kiran
; APPLICANT: Folkerts, Otto
; APPLICANT: Martin, Gregory
; APPLICANT: Ekengren, Sophia
; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGE
; TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE
; FILE REFERENCE: BTI.67A2
; CURRENT APPLICATION NUMBER: US/10/341,961A
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: 60390249
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60261029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60348792
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 371
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-341-961A-371

Query Match 18.8%; Score 291.2; DB 16; Length 510;

Best Local Similarity 78.1%; Pred. No. 6.8e-54;

Matches 350; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 ATCTTTGTTTGAATAAATTTGGAAGAACGCTAGGACCAATGGACCTTGGGTGCAACAAT 60
Db 448 ATCTTTGTTTGAATAAATTTGGAAGAACGCTAGGACCAATGGACCTTGGGTGCAACAAT 389
QY 61 ATTTGTTGCTTCCAAATGTGTACAAGGATTTTACATCTCTCGGCTACTTTAAAGCTGAC 120
Db 388 ATTTGTTGCTTCCAAATGTGTACAAGGATTTTACATCTCTCGGCTACTTTAAAGCTGAC 329
QY 121 TAGGACATTCACCATTTATTTTCCGCTGCATTTGAATGCTGCTGATTCCTCCACTTG 180
Db 328 CAGGCAATTCACCGTTTATTTTGTGCTGTCATTTGAATGCTGATGATGATTTTCCAGGGCCAG 269
QY 181 GATTAGTCCGGGCGAAAGTCTATCGGTATATTTAAATCCATCAACTAAAGAAATGTCCAG 240
Db 268 GCTTAGTTGGCCAAAGACATAGGATTTTGAATCCATCAATAACAGAAATATCCCAA 209
QY 241 AATCTAAGTTTGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 208 AATCTAAGTTTGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 149
QY 301 ACCCGGTGCTAGCTGAGGACCAACCAATCACCAGTCTATGCAAGCACTTACACCACTTAC 360
Db 148 ATCTTTTGTGAATCAGGATCTCCACCAATCAGATCTGACCACTTCTTCCAGCAC 89
QY 361 CATCGAAGTTTACATCCAGTACGACCCCATATAGTGCATGCTAGTGTCCCTTACGGCCAT 420
Db 88 CATCAAGTTTGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 29
QY 421 CAATGACCCAGTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 448
Db 28 AAAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1

RESULT 5

US-05-938-842A-2118/c

; Sequence 2118, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2118
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2118

Query Match 13.4%; Score 207.2; DB 9; Length 735;
Best Local Similarity 64.6%; Pred. No. 2.4e-35;
Matches 346; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

Qy 43 GACCTTGGGTGCAACAATATTGTTGCTCTCCAAATGGGTACAGGATTTGTTACATCCTC 102
Db 535 GACCGTTTCGTACACAGTATTGGTTCGTAATAACAGTACACGGGTGTTGTCATCCAC 476

Qy 103 CGGTACTTTAAGCTGACTAGGACATTCACATTTATATTGCGTGCATTTGAATTCGCT 162
Db 475 CTGGGGCTCTCAACACGTTTGGACATTTGCGTTTATGTTCTGCGGTACATAGTATCCGAT 416

Qy 163 GGCATTTCCCTCCACTTGGATTAGTCGGGGGAAAGTCATCGGTATATTAAATCCATCAA 222
Db 415 GGCAGTTC-----GAACTAGTTGGCTAAACTCCTAGGTATGTTTAAATCCATCGA 365

Qy 223 CTAAAGAAATGTCGCCAAGAAATCTAAGTTGTTGAATCTGGTCCGAGCGGTACTCGGCTAGGG 282
Db 364 CAAGTGAGATATCGTAGAAGTCTAAGTTGTTGAATTTGTTCAAGCGTACTCAGCCAAACG 305

Qy 283 TGTGTTGGGTTTACCCACCGGTGCACTGCAGGACACCAACCAATCCAGTCAATGC 342
Db 304 TGTGTTGGGTTGTTCCCGAGCGGTACATTTGGATGTCACCACTGCATGCTACCAAGTTGGC 245

Qy 343 ACGAACTCTACAGCACCATCGAAGTTTACATCCAGTACGACCCCATATATACGTGCCATCG 402
Db 244 ATCGGCCACGACCTGAGGAGTCAAAGTTTACAAATGGTCTTACCCCAAATCCGTGCCATTT 185

Qy 403 TAGTGCCCTTAGGCGCATCAATGACCCAGTTTGGCTCGATCGAGACGTGCGCCACCGC 462
Db 184 TAGTGCCCGCGCGACATCTAGCCTTCCATGATTTGCGCCAGCATCTAGACGTGCGCCACCTC 125

Qy 463 CTATCGGGTTCGATGTCGCCAGACGGGTATGACAGTGTGTTGGTACTCTCGATAGTGG 522
Db 124 C---AGGGCTTGGCGAGCCACACGGTGTAACTACTATTGTTAGGATTTGCAATGTGG 68

Qy 523 CAGCATATAGTGAAGTCAAAAGCAAGAGGAGGAGAAACAAAAGAGATCTCAAG 578
Db 67 CGGCTGTTGCGGTGGAGATGAGCAAAAGTGGGAAATATGAAAGTAGAGACCAAG 12

RESULT 6
US-09-938-842A-2118/c
; Sequence 2118, Application US/09938842A
; Publication No. US2004009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepes, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2118
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2118

Query Match 13.4%; Score 207.2; DB 11; Length 735;
Best Local Similarity 64.6%; Pred. No. 2.4e-35;
Matches 346; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

Qy 43 GACCTTGGGTGCAACAATATTGTTGCTCTCCAAATGGGTACAGGATTTGTTACATCCTC 102
Db 535 GACCGTTTCGTACACAGTATTGGTTCGTAATAACAGTACACGGGTGTTGTCATCCAC 476

Qy 103 CGGTACTTTAAGCTGACTAGGACATTCACATTTATATTGCGTGCATTTGAATTCGCT 162
Db 475 CTGGGGCTCTCAACACGTTTGGACATTTGCGTTTATGTTCTGCGGTACATAGTATCCGAT 416

Qy 163 GGCATTTCCCTCCACTTGGATTAGTCGGGGGAAAGTCATCGGTATATTAAATCCATCAA 222
Db 415 GGCAGTTC-----GAACTAGTTGGCTAAACTCCTAGGTATGTTTAAATCCATCGA 365

Qy 223 CTAAAGAAATGTCGCCAAGAAATCTAAGTTGTTGAATCTGGTCCGAGCGGTACTCGGCTAGGG 282
Db 364 CAAGTGAGATATCGTAGAAGTCTAAGTTGTTGAATTTGTTCAAGCGTACTCAGCCAAACG 305

Qy 283 TGTGTTGGGTTTACCCACCGGTGCACTGCAGGACACCAACCAATCCAGTCAATGC 342
Db 304 TGTGTTGGGTTGTTCCCGAGCGGTACATTTGGATGTCACCACTGCATGCTACCAAGTTGGC 245

Qy 343 ACGAACTCTACAGCACCATCGAAGTTTACATCCAGTACGACCCCATATATACGTGCCATCG 402
Db 244 ATCGGCCACGACCTGAGGAGTCAAAGTTTACAAATGGTCTTACCCCAAATCCGTGCCATTT 185

Qy 403 TAGTGCCCTTAGGCGCATCAATGACCCAGTTTGGCTCGATCGAGACGTGCGCCACCGC 462
Db 184 TAGTGCCCGCGCGACATCTAGCCTTCCATGATTTGCGCCAGCATCTAGACGTGCGCCACCTC 125

Qy 463 CTATCGGGTTCGATGTCGCCAGACGGGTATGACAGTGTGTTGGTACTCTCGATAGTGG 522
Db 124 C---AGGGCTTGGCGAGCCACACGGTGTAACTACTATTGTTAGGATTTGCAATGTGG 68

Qy 523 CAGCATATAGTGAAGTCAAAAGCAAGAGGAGGAGAAACAAAAGAGATCTCAAG 578
Db 67 CGGCTGTTGCGGTGGAGATGAGCAAAAGTGGGAAATATGAAAGTAGAGACCAAG 12

RESULT 7
US-09-770-445-334/c
; Sequence 334, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja

; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith
 ; APPLICANT: Hoffman, Neil
 ; APPLICANT: Hurban, Patrick
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; TITLE OF INVENTION: thaliana
 ; FILE REFERENCE: 2023US (PARA-012PRV)
 ; CURRENT APPLICATION NUMBER: US/09/770,445
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: US 60/178,472
 ; PRIOR FILING DATE: 2000-01-27
 ; NUMBER OF SEQ ID NOS: 999
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 334
 ; LENGTH: 950
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-770-445-334

Query Match 13.4%; Score 207.2; DB 9; Length 950;

Best Local Similarity 64.6%; Pred. No. 2.8e-35;
Matches 346; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

QY 43 CACCTTGGGTGCAACAATATTTGTTCTCTCCAAATGTGTACAGGATTTGTTACATCCTC 102
 DB 543 GACCGTTGCTACACAGATTTGTTCTGCTGAATACAGTACACGGGTTGTTGATCCAC 484
 QY 103 CGGTACTTTAAGTGTACTAGCAATTCACATTTATTTATTTGCGGTGCAATTTGCGGT 162
 DB 483 CTGGGGCTCTCAACACGCTTTGGACATTTGCTGCTTATTTGCTGCGGTACATAGTATCCGAT 424
 QY 163 GGCATTTTCCCTCCACTTGGATTACTCGGGGCAAGTATCGGTATTTAAATCCATCAA 222
 DB 423 GCGAGTTTCT-----GACATGTTGGGCTAAACTCCATAGGTATTTAAATCCATCGA 373
 QY 223 CTAAGAAATATGCCCAAAATCTAAGTTGTTGAATCTGTCGAGGGGTACTCGGCTAGGG 282
 DB 372 CAAGTGAGATATCTAGAAGTCTAAGTTGTTGAATGTTTCAAAGGCTACTCAGCCAACG 313
 QY 283 TGTGTTGGGTTTACCCCAACCGGTGCACTGCAGGACACCAACATCACCAGTCAATCG 342
 DB 312 TGTGTTGGGTTGTCCTCCAGCCAGTCAATGGAGTCCACACTGCAGTCAACAGTTTGGC 253
 QY 343 ACGAACCTCTACAGCAACCATCGAAGTTATACATCCAGTACGACCCCATATACGTGCGCATCG 402
 DB 252 ATCGGCCACGACCTGAGGAGTCAAGTTACAATTTGTTCTTACCCCAATCCGTGCCATTT 193
 QY 403 TAGTGGCCCTAGGGGATCAATGACCAACGTTTGGGCTCGATCGAGAGTGGGCCACCGC 462
 DB 192 TAGTGGCCCGCGGACATCTAGCTCTCCATGATTTGGCCAGCATCTAGACGTTCGSCCACTC 133
 QY 463 CTATCGGGGTGATGCTGCTCCAGACGCTGATGAGACAGTTGTTGCTGATGATGCG 522
 DB 132 C---AGGGCTTGGGACGCCCAACGCTGTAATCTATTTGTTAGATTTGATGTTGG 76
 QY 523 CAGCATTAAGTGAAGTCAAAAAGCAAGAGGAGGAGAAAACAAAAGAGATCTCAAG 578
 DB 75 CGGCTGTTGGGTGGAGATGAGCAAAAGTCCGGAATAATATGAAGTAGAGACCAAG 20

RESULT 8

US-10-424-599-103619/c
 ; Sequence 103619, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 103619
 ; LENGTH: 909
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_64586C.1
 US-10-424-599-103619

Query Match 11.8%; Score 182.4; DB 13; Length 909;

Best Local Similarity 61.4%; Pred. No. 7.8e-30;
Matches 329; Conservative 0; Mismatches 201; Indels 6; Gaps 2;

QY 1 ATCTTTGTTGAAAAAATTGGAAAAAGACGTAGGACACATGACCTTGGGTGCAACAAT 60
 DB 628 ACCTTTGCTTGAAGATCTGGAATTAATCAGTGGGCCCACTACCGGAATTGCAACAGT 569
 QY 61 ATGTGTGCTCTCCAAATGTGTGTAAGGATTTTACATCTCTCGGGTACTTTAAGCTGAC 120
 DB 568 ACTGTCGCGTTTGAAGACAGTGCAGAGGTTGTTGCAACCTCTTGAAGTCTTTAGCTCAC 509
 QY 121 TAGGACATTCACCATTTATATTTCCGTCGTCATTGAATTCGTCGTCATTTCCCTCCACTTG 180
 DB 508 TAGGCACTGTCGCTTAATGTCGCGAGTGCA---GCTTATGCCACGTGTGATCCATTCG 452
 QY 181 GATTAGTCCGGGCGAAGTCAATCGGTATATTTAAATTCATCACTAAAGAAATGTCGCCAGA 240
 DB 451 ---AGTTGGACTAAAGTCCATGCGCAGCTTTAAACCGTCGACGAGGAGATGTCGAAGA 395
 QY 241 RATCTAAGTCTGTAAGTCTGTCGAGGCGTACTCGGCTAGGCTGTTGGCGGTTTACCCC 300
 DB 394 AGTCAAAATTTGTAACCCGTTTACGCGCGGTATTGAGCCAGGGTGTGGGAGGCGCACCGT 335
 QY 301 ACCCGGTGCACTGCAGGACACACACAATCACCAGTCACTGCAGAACTCTACAGCAC 360
 DB 334 AAGCTTTCAGTGCAGGACACACCCCGGAGTACACCGTCTGTCATCCACCGGCGCCGAAC 275
 QY 361 CATCGAAGTACATCCAGTACGACCCCATATACGTGCCATGCTAGTGCCTTAGGCGCAT 420
 DB 274 CGTGAAGTTTCAGCCGCTTCCGGCCCCAAACCGCGGCCCCCTTTCTGTTCTGTCAGSCACGT 215
 QY 421 CAATGACCCACGTTTGGCTCGATCGAGACGTGCGGCCACCGCTATCGGGTGTGATGCTG 480
 DB 214 CCACGGACCATGACTGCGCCGGGTTTAATTGACGCCACCGCCCAAGGACACAGCGAG 155
 QY 481 CCCAGACGTTGATGAGACAGTGTGTCGTACCTCGATAGTGGGACGATTAAGTGAAG 536
 DB 154 CCCAGACGTTGATGTCATCGGTTTGTGATTTCAAACTTGCAGCATATGCGGAA 99

RESULT 9

US-10-636-396-4/c
 ; Sequence 4, Application US/10636396
 ; Publication No. US20040073971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Crasta, Oswald R.
 ; APPLICANT: Duwick, Jon
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guihua
 ; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
 ; TITLE OF INVENTION: Genes and their Uses
 ; FILE REFERENCE: 5718-90
 ; CURRENT APPLICATION NUMBER: US/10/636,396
 ; CURRENT FILING DATE: 2003-08-07
 ; PRIOR APPLICATION NUMBER: US/09/589,733C
 ; PRIOR FILING DATE: 2000-06-08
 ; PRIOR APPLICATION NUMBER: 60/140,646
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/162,904
 ; PRIOR FILING DATE: 1999-11-01

```

; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-10-636-396-4

Query Match      11.7%; Score 180.6; DB 12; Length 875;
Best Local Similarity 60.9%; Pred. No. 1.9e-29;
Matches 332; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

QY 1 ATCTTTGTTTGAAGAAATTTGAAAGACGTAGGACACATGGACCTTGGGTGCAACAAT 60
Db 577 ATCTGGCTTGAAGAAACCTTGATTAATCAGTTGGTCCAAATTTCCAGAGTTGCACAT 518
QY 61 ATTGTTGTCCTCCAAATGTTGTAAGATTTTACATCTCCGGGTACTTTAAGCTGAC 120
Db 517 ACTGATCAGTTTGTACAGGTGCAAGGTTATTGCAACCCGACAGGACCCGTAATCAC 458
QY 121 TAGGACATTCACCAATTTATTTTCCGTCGATTTGCGTGGGATTTCCCTCCACTTG 180
Db 457 CAGGACATCGGCCATTGATATCCGCAGTACATGAGATACCCCGGTGCACCC-----AT 404
QY 181 GATTAGTCGGGGCGAAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGTCCAGA 240
Db 403 TAGAATTCGGTCTAAACACCAATCGGCACATTTGAATCCGTCACACAGAGAAATGTCAAAGA 344
QY 241 AATCTAAGTTTGTGAATCTGGTCCGAGGCGTACTCGGTAGGTTGTTGGCGGTTTACCCC 300
Db 343 AATCAAGATTGTGAATCTGGTTCAAAGCGTACTCGGCCAATGTGTGGGTGGGTACCAT 284
QY 301 ACCCGTGCATCGAGGACACCAATCAATCAGCATGATCAGCAACCTTACACGAC 360
Db 283 AGTTTGGCATTTGGAGAGACCGTTTGCATCACCCTCTGACACCTGCTCCGCGCAAC 224
QY 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTCCCATCGTCCCATAGGCGCAT 420
Db 223 CATCAAGTTGCAATTTGTTCCGGGCCATATACGGCTCTGTCGACCTGCGCGG 164
QY 421 CAATGACCCAGTTTGGCTCGATCGAGCTCGGCCACCGCTATCGGGTTCATGCTG 480
Db 163 TTAAGACACAGTTTGGCTCGATTAAGTTGTGGCGCCGACCC---AGGCACCCGAC 107
QY 481 CCCAGACGTTGATGACAGTTTGTTCGTCATGTCGACGATGTCGACGATGAAAGTCA 540
Db 106 CCCAAGCGTTATGACAGTTGTTTCGAATAGTGAACACGCGTGCATTGGTATAGTAA 47
QY 541 CAAAA 545
Db 46 AAAGA 42

```

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RESULT 10
US-10-636-026-4/c
; Sequence 4, Application US/10636026
; Publication No. US20040111761A1
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Ducrest, Jon
; APPLICANT: Duvick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; TITLE OF INVENTION: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/10/636,026
; PRIORITY FILING DATE: 2003-08-07
; PRIOR FILING DATE: 2000-06-08
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR APPLICATION NUMBER: 60/162,904

```

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; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-10-636-026-4

Query Match      11.7%; Score 180.6; DB 17; Length 875;
Best Local Similarity 60.9%; Pred. No. 1.9e-29;
Matches 332; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

QY 1 ATCTTTGTTTGAAGAAATTTGAAAGACGTAGGACACATGGACCTTGGGTGCAACAAT 60
Db 577 ATCTGGCTTGAAGAAACCTTGATTAATCAGTTGGTCCAAATTTCCAGAGTTGCACAT 518
QY 61 ATTGTTGTCCTCCAAATGTTGTAAGATTTTACATCTCCGGGTACTTTAAGCTGAC 120
Db 517 ACTGATCAGTTTGTACAGGTGCAAGGTTATTGCAACCCGACAGGACCCGTAATCAC 458
QY 121 TAGGACATTCACCAATTTATTTTCCGTCGATTTGCGTGGGATTTCCCTCCACTTG 180
Db 457 CAGGACATCGGCCATTGATATCCGCAGTACATGAGATACCCCGGTGCACCC-----AT 404
QY 181 GATTAGTCGGGGCGAAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGTCCAGA 240
Db 403 TAGAATTCGGTCTAAACACCAATCGGCACATTTGAATCCGTCACACAGAGAAATGTCAAAGA 344
QY 241 AATCTAAGTTTGTGAATCTGGTCCGAGGCGTACTCGGTAGGTTGTTGGCGGTTTACCCC 300
Db 343 AATCAAGATTGTGAATCTGGTTCAAAGCGTACTCGGCCAATGTGTGGGTGGGTACCAT 284
QY 301 ACCCGTGCATCGAGGACACCAATCAATCAGCATGATCAGCAACCTTACACGAC 360
Db 283 AGTTTGGCATTTGGAGAGACCGTTTGCATCACCCTCTGACACCTGCTCCGCGCAAC 224
QY 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTCCCATCGTCCCATAGGCGCAT 420
Db 223 CATCAAGTTGCAATTTGTTCCGGGCCATATACGGCTCTGTCGACCTGCGCGG 164
QY 421 CAATGACCCAGTTTGGCTCGATCGAGCTCGGCCACCGCTATCGGGTTCATGCTG 480
Db 163 TTAAGACACAGTTTGGCTCGATTAAGTTGTGGCGCCGACCC---AGGCACCCGAC 107
QY 481 CCCAGACGTTGATGACAGTTTGTTCGTCATGTCGACGATGTCGACGATGAAAGTCA 540
Db 106 CCCAAGCGTTATGACAGTTGTTTCGAATAGTGAACACGCGTGCATTGGTATAGTAA 47
QY 541 CAAAA 545
Db 46 AAAGA 42

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RESULT 11
US-10-424-599-36321/c
; Sequence 36321, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 36321
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Glycine max

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FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1956)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_132800C.1
US-10-424-599-36321

Query Match 11.1%; Score 171.6; DB 13; Length 1956;
Best Local Similarity 59.8%; Pred. No. 2.8e-27;
Matches 329; Conservative 0; Mismatches 209; Indels 12; Gaps 2;
QY 39 CATGACCTTGGGTGACACAAATATTGTTGCTCTCAAAATGGTGTACAGGATTTGTTACAT 98
Db 1290 CTTGCCCATTTGGTGCAGCAATCTCAATTCGTTCTTAAACACAGTGCAGGGGTTGTTGCAT 1231
QY 99 CTTCCGGGTACTTTAAAGCTGACTAGACATTCACCAATTTATTTGCGGTGCAATTTGAAT 158
Db 1230 CCCCAGGTGCCCTTAATGGCCCCGGGCACTGCCCAATTTGATATCAGCGCTCAACTGAT 1171
QY 159 GGTGGCAATTCCTCCACTTGGATTAGTCGGGGGGAAGTCATCGGTATATTAATCCA 218
Db 1170 TTGTGACACCCACCG-----TTTAGAGGTAGAAAGTCCATCGGAATGTTGAACCG 1120
QY 219 TCAACTAAAGAAATGCTCCAGAAATCTAAGTTGTTGAAGTGGTCCGAGGGTACTCGCT 278
Db 1119 TCACCAAGAGATGCTGTAAGATCTGTTGCAATTTGGTTGCAATTTGGTTCAACGGGAATTCGCA 1060
QY 279 AGGTGTTTGGCGGTTTACCCACCCCGGTGCACTGCAGGACACCAACCAATCACCAGTC 338
Db 1059 AGTGTGTTGGGAGGACCCCGGCTTGGCAATTTAGGCGCGCGTCACTCCCGTT 1000
QY 339 ATGCAGCACTCTACAGACCACTAGAGTTAGATTCAGTACGACCCCATATACGTGCC 398
Db 999 TGGCAGCGCGCGCGCGCTCCCTCAAAAGTTGACCGGTGCGCGGCGCCCATATACGGGCC 940
QY 399 ATCGTAGTCCCTAGGCGGATCAATGACCCACGTTTGGCTCGATCGAGACGTCGSCCA 458
Db 939 ATGCAGTGCCTGGGTTTACCCAGAGTTTCAAGTTTGGCCAGCTTCAAGCGCGGCT 880
QY 459 CCGCTATCGGGTGCATGTCGCCAGACCGGTGATGAGCAAGTTTGGCTGCTGCTGATA 518
Db 879 CCACC---CGGACTCGCGCGCGCCACACCGTGTAGGGGCAATTTGTGAGCATCTCGAAG 823
QY 519 GTGCAGCATAGTGAAGTACAAAAGCAAGAGGAGGAGGAGAAACAAAGAGATCTCAAG 578
Db 822 TTTCAGCATGATTTGTTGCCAAGGTAAGGCCAACGTTAGCAGAGACAGTGCACAG 763
QY 579 TAGCCCATGT 588
Db 762 TAAACCATTT 753

RESULT 12
US-10-259-165-389/c
; Sequence 389, Application US/10259165
; Publication No. US2003013588A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCES: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165

; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 389
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-389
Query Match 10.1%; Score 155.8; DB 15; Length 717;
Best Local Similarity 57.9%; Pred. No. 4.8e-24;
Matches 297; Conservative 0; Mismatches 212; Indels 4; Gaps 1;
QY 50 GGTGCAACAAATATTGTTGCTCTCCAAATGTGTACAAAGGATTTTACATCTCCCGGTAC 109
Db 541 GGTGCAGCAGTACTGTCCTGCTTGAACACCGTGCACGGTGTGTCACCGCGGGCGC 482
QY 110 TTTAAGCTGACTAGGACATTCACCAATTTATTTGCGGTGCAATTTGAATTTGG 165
Db 481 CTTGAGTCTGCTCGGGCACTGCCCCCGCCACCGTCCGCTCGCACCGCGCGCCCTTGGC 422
QY 166 ATTTCCCTCCACTTGGATTAGTCGGGGGAAAGTCTATCGGTATATTAATTCATCACTA 225
Db 421 GCACCGCGCGCTGCGCGCGGGGAGGAGTCCATGCGCACGTTGAATTCGTGATGA 362
QY 226 AAGAAATGTCAGAAATCTAAGTTGTTGAATCTGTCGAGGCGTACTCGGCTAGGGTGT 285
Db 361 GGGAGATGTGCAAGAAAGTCTGAGTTGCTGAACTGTTTCAAGCGCAACTCCCGCAGCGTGT 302
QY 286 TTGGCGGTTTACCCACCCCGGTGCACTGCAGGACACCAACCAATCACCAGTCATGACG 345
Db 301 TGGGCGGTGTCCTGCTGACCGCGGACCGAGCAGCGCGCGGCTGCTGCGGCTTGGCACC 242
QY 346 AACCTCTACAGCACCATCGAAGTTTACATTCAGTACGACCCCATATACGTGCCATCGTAG 405
Db 241 GCCCGTTGCGGTGCGGTGCAAGTCTGAGCGCGTGCAGCGCCACACGCGCGCGCGCTCG 182
QY 406 TCGCCCTAGGCGCATCAATGACCCACGTTTGGCTCGATTCAGAGCTCGGCGCACCGCTA 465
Db 181 TCGCGCGCGGACGTCGATCACCACACTGCTGCCCGGGTCCAGTGTGCTGCCCGCGCGG 122
QY 466 TCGGGTTCGATGCTGCCCGAGCGGTGTATGACACAGTTGTTTCGTACCTCGATAGTGGCAG 525
Db 121 ACGGCACGCTGCCCGCCACACGCGTGTCTGGCACTTGTGTTGTTGTTGTTGTTGTTGTTG 62
QY 526 CATAAGTGAAGTCAAAAGCAAGAGAGGAGA 558
Db 61 CGTTCCGCGCGCGCGAGGAGAGAGAGGA 29

RESULT 13
US-10-259-165-41/c
; Sequence 41, Application US/10259165
; Publication No. US2003013588A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell

;; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
;; FILE REFERENCE: 70030-NP
;; CURRENT APPLICATION NUMBER: US/10/259,165
;; PRIOR FILING DATE: 2002-09-26
;; PRIOR APPLICATION NUMBER: US 60/370,620
;; PRIOR FILING DATE: 2002-04-04
;; PRIOR APPLICATION NUMBER: US 60/369,327
;; PRIOR FILING DATE: 2002-03-27
;; PRIOR APPLICATION NUMBER: US 60/325,277
;; PRIOR FILING DATE: 2001-09-26
;; NUMBER OF SEQ ID NOS: 782
;; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
;; SEQ ID NO 41
;; LENGTH: 720
;; TYPE: DNA
;; ORGANISM: Oryza sativa
;; US-10-259-165-41

Query Match 10.1%; Score 155.8; DB 15; Length 720;
Best Local Similarity 57.9%; Pred. No. 4.9e-24;
Matches 297; Conservative 0; Mismatches 212; Indels 4; Gaps 1;
QY 50 GGTGCAACAATTTGTTGCTCCCAATGTTGGTACAGGATTTTACATCTCCGGGTAC 109
DB 541 GGTGCAACAATTTGTTGCTCCCAATGTTGGTACAGGATTTTACATCTCCGGGTAC 482
QY 110 TTTAAGCTGACTAGGACATTCACCAATTTATTTTGGTGTGATTTGAATTTGGC 165
DB 481 CCTCAGCTCGTCCGGCACTCCCGCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 422
QY 166 ATTTCCCTCCATCTGGATTAATCGGGGCAAGTATCGGTATATTTAAATCCATCACTA 225
DB 421 GCACCCGCGCGCTGCGCGCGCGGGGAGGAAAGTCCATGGGACGCTTGAATCCGTCGATGA 362
QY 226 AAGAAATCTCCAGAAATCTAAGTTTGAATCTGTCGAGCGCTACTCCGGCTAGGGTGT 285
DB 361 GGGAGATGTCGAAGAAGTCGAGTTGCTGAATGTTGTCAGCGCAACTCCCGCAGCGTGT 302
QY 286 TTGGCGGTTTACCCACCCCGGTGCACTCCAGGACACCAACCAATCAACGATCANGCAG 345
DB 301 TGGCGGCTGCGCGTACGCGCGCACCGCGCAGCAGCGCGCGCGCTCTGGCACC 242
QY 346 AACCTCTACGACCACTCGAATTTACATCCAGTACGACCCCATATAGTSCCATCTAG 405
DB 241 GCCCGTTCGCGTCCGCTGCGAGCTGTCAGCGCGCTGCGCGCCCAACGCGCGCGCGCTG 182
QY 406 TGCCCTTAGGGCGCATCAATGACCCACGTTTGGCTTCGATCGAGACGTGCGGCCACCGCTA 465
DB 181 TGCCCGCGGACGTCGATCACCCTGCTGCGCGGCTCCAGCTGCTGCGCGCGCGCG 122
QY 466 TGCGGGTCGATGCTCCCGACGCGTGTATGACAGTTGTTGGTACCTCGATAGTGGCAG 525
DB 121 ACGGCACGCGCTGCGCGCCCAACGCGTGTCTGGCACTTGTGATGTTGTAACGTTGCGG 62
QY 526 CATNAGTGAAAGTCAAAAGCAAGAGGAGGA 558
DB 61 CTTTCGCGCGCGCGGAGGAGGAGAGAGGGA 29

RESULT 14
US-10-437-963-86607/c
; Sequence 86607, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;; FILE REFERENCE: 38-21(53221)B
;; CURRENT APPLICATION NUMBER: US/10/437,963
;; CURRENT FILING DATE: 2003-05-14
;; NUMBER OF SEQ ID NOS: 204966
;; SEQ ID NO 86607
;; LENGTH: 1006
;; TYPE: DNA
;; ORGANISM: Oryza sativa
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT4530_85631C.1
;; US-10-437-963-86607

Query Match 9.9%; Score 153.6; DB 17; Length 1006;
Best Local Similarity 57.6%; Pred. No. 1.8e-23;
Matches 295; Conservative 0; Mismatches 214; Indels 3; Gaps 1;
QY 50 GGTGCAACAATTTGTTGCTCCCAATGTTGGTACAGGATTTTACATCTCCGGGTAC 109
DB 584 GGTGCAACAATTTGTTGCTCCCAATGTTGGTACAGGATTTTACATCTCCGGGTAC 525
QY 110 TTTAAGCTGACTAGGACATTCACCAATTTATTTTGGTGTGATTTGAATTTGGC 166
DB 524 CCTCAGCTCGTCCGGCACTCCCGCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 465
QY 167 TTTCCCTCCATCTGGATTAATCGGGGCAAGTATCGGTATATTTAAATCCATCACTAA 226
DB 464 GCACCCGCGCGCTGCGCGCGGGGAGGAAAGTCCATGGGACGTTGAATCCGTCGATGAG 405
QY 227 AGAAATGTCGCAAAATCTAAGTTTGAATCTGTCGAGCGGTACTCCGGCTAGGGTGT 286
DB 404 GGGATGTCGAAGAAGTCGAGTTGCTGAATGTTTTCAGGCGCACTCCCGCAGCGTGT 345
QY 287 TGCGGTTTACCCACCCCGGTGCACTTCGAGGACACCAACCAATCAACGATCANGCAG 346
DB 344 GGGCGGCTGCGCGTACGCGCGCACCGCGCAGCAGCGCGCGCGCTCCCGCTCTGGCACC 285
QY 347 ACCTCTACGACCACTCGAATTTACATCCAGTACGACCCCATATAGTSCCATCTAG 406
DB 284 CCGTTTCCGCTCCGCTGCAAGCTGCAAGCTGCGCGCGCCCAACGCGCGCGCGCTGCT 225
QY 407 GCGGCTAGGCGCATCAATGACCCACGCTTTGGCTTCGATCGAGACGTGCGGCCACCGCTAT 466
DB 224 GCGGCGCGGACGCTCGATCACCCTGCTGCGCGGCTCCAGCTGCTGCGCGCGCGCG 165
QY 467 CGGGTTCGATGCTGCGCGCGCGGTGATGGACAGTTGTTGGTACCTCGATAGTGGCAG 526
DB 164 CGGACGCGCTGCGCGCCCAACGCGTGTCTGGCACTTGTGATGTTGTAACGTTGCGGCG 105
QY 527 ATAAGTGAAAGTCAAAAGCAAGAGGAGGA 558
DB 104 GTTCGCGCGCGCGGAGGAGGAGAGGGA 73

RESULT 15
US-10-424-599-7736/c
; Sequence 7736, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 7736
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Glycine max

; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ..(1173)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_106998C.1
US-10-424-599-7736

Query Match 9.4%; Score 145.4; DB 13; Length 1173;
Best Local Similarity 58.5%; Pred. No. 1.2e-21;
Matches 320; Conservative 0; Mismatches 206; Indels 21; Gaps 3;
QY 1 ATCTTTGTTTGAAGAAATGAAAGAACGTAGGACCACA-----TCGACCTTGGGTGC 54
Db |||||
664 ACCTCTCTTTGAGAACTTGGAAATATCATGTGGACCGCAACCCGAGCACCCTGCTAC 605
QY 55 AACAAATATTTGTCCTCCAAATGTGGTACAAAGATTTTACATCTTCGGGTACTTTAA 114
Db |||||
604 AACAGTACTGATCGTATTGAAACCGTGCACGGGTGTTGCAGCGCGGGAACTGAA 545
QY 115 GCTGACTAGGACATTCACCATTTATTTGCGGTGCATTTGAATTCGTCGCAATTCCTC 174
Db |||||
544 GCTGAGTGGACACTCTCCGATGATGTCGGCGGCGCATTTCCGAGCTGCAGTTG--- 489
QY 175 CACTTGGATTAAGTCGGGCGAAAGTCAATCGGTATATTAATTCATCAACTAAAGAAATGT 234
Db |||||
488 -----TAGGTGGGCTCACCTGCAAGGGAATGTTGAAACCGTGCACGAGGAGATGT 437
QY 235 CCCAGAAATCTAAGTTGTTGAATCTGTCGAGGCGGTACTCGGCTAGGGTGTTCGGCGGT 294
Db |||||
436 CGTAAAGTCGAGGTGTTGTACTGGTTCACCGGGAATTCACCAACGTGTTCGGAGGTG 377
QY 295 TACCCACCCCGTGCACCTGCAGGACACCAACACATCACCAGTCAATGCACGAACCTCTAC 354
Db |||||
376 TACCTGTTTTTGTGACTCAAGACACCGTCGAGTCGCGGTGAGGCACTTCCCGGTC 317
QY 355 CAGCACCATCGAAGTTACATCCAGTACGACCCCATATACGTGGCATCGTAGTCCCTAG 414
Db |||||
316 CTGGTTTGTGCAAGGTGAGTTTTCGACCCAGATCGCTCTCTCTGTCGTCGCTCG 257
QY 415 GCGCATCAATGACCCAGCTTTGGCTCGATCGAGAGCTGCGCACCGCCTATCGGGTGC 474
Db |||||
256 TCACGCTGATTTCCAGATTCGCGAGGTTAGCCTTGAGCCGCCGCC---GGGACGG 200
QY 475 ATGCTGCCAGACGGTGTATGACAGTGTGTGGTACCTCGATAGTGGCAGCATAAAGTGA 534
Db |||||
199 CGCGGCCCCACACCGTGTAGTGCAATTTGTTGATGTTGAAGTTGCTGCTGCTGAGCTA 140
QY 535 AAGTCAC 541
Db |||||
139 CGGCCAC 133

Search completed: August 18, 2004, 16:52:41
Job time : 682.862 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 05:06:40 ; Search time 3634.85 Seconds
(without alignments)
12701.209 Million cell updates/sec

Title: US-10-051-307-3

Perfect score: 1546

Sequence: 1 atcttctttgaaaaaattg.....tggagaagtgggtgcttc 1546

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_fod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	505.2	32.7	899	14	CK252883 EST736520
C 2	505.2	32.7	1004	14	CK248798 EST732435
C 3	502	32.5	988	14	CK246326 EST729963
C 4	500.2	32.4	888	14	CK278032 EST724110

C 5	499.6	32.3	853	14	CK271811
C 6	499.2	32.3	899	14	CK252271
C 7	495.8	32.1	739	12	BI176339
C 8	490.2	31.7	649	9	AW039873
C 9	487.2	31.5	583	12	BI432833
C 10	486	31.4	622	10	BF053678
C 11	485.2	31.4	639	12	BGI30690
C 12	483	31.2	667	12	BI922472
C 13	480.8	31.1	585	9	AW031249
C 14	474.6	30.7	923	14	CK273930
C 15	474.4	30.7	593	9	AW032915
C 16	472.2	30.5	777	12	BM407898
C 17	471.4	30.5	651	10	AW218785
C 18	469.4	30.4	586	9	AW033588
C 19	469.4	30.4	649	10	AW222204
C 20	469.4	30.4	652	12	BI922170
C 21	469.4	30.4	669	12	BI921735
C 22	469.4	30.4	782	12	BM410787
C 23	467.2	30.2	944	14	CK271145
C 24	466.2	30.2	598	14	CA514039
C 25	462.8	29.9	936	14	CK277819
C 26	461.2	29.8	916	14	CK279273
C 27	461	29.8	638	12	BI434454
C 28	461	29.8	757	12	BI434095
C 29	460.4	29.8	657	10	AW223507
C 30	457.8	29.6	660	12	BM403979
C 31	457.2	29.6	776	12	BGI23660
C 32	457.2	29.6	575	12	BI421330
C 33	456.2	29.5	574	10	AW441774
C 34	455.4	29.5	604	12	BI423179
C 35	455.4	29.5	637	12	BI921311
C 36	455.4	29.5	719	12	BI422260
C 37	455.4	29.5	720	12	BI921826
C 38	455.4	29.5	807	12	BI421946
C 39	454.6	29.4	574	10	AW223623
C 40	454.4	29.4	626	9	AW033829
C 41	453.8	29.4	629	10	BE432710
C 42	453.8	29.4	635	12	BM403950
C 43	453.4	29.3	682	10	AW223970
C 44	453.4	29.3	710	9	AW035171
C 45	453.2	29.3	573	9	AW032317

ALIGNMENTS

RESULT 1
LOCUS CK252883/c 899 bp mRNA linear EST 12-DEC-2003
DEFINITION EST736520 potato callus cdna library, normalized and full-length
Solanum tuberosum cdna clone POC0086 5' end, mRNA sequence.
ACCESSION CK252883
VERSION CK252883
KEYWORDS EST, GI:39807285
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 899)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE Generation of ESTs from potato callus tissue
JOURNAL Unpublished (2003)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTC ACA CTA TAG.

FEATURES
source

Location/Qualifiers
1..899
/organism="Solanum tuberosum"
/mol_type="mRNA"

/cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="POC086"
 /tissue_type="callus"
 /lab_host="DH10B-Tona"
 /clone_lib="potato callus cDNA library, normalized and full-length"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

ORIGIN

Query Match 32.7%; Score 505.2; DB 14; Length 899;
 Best Local Similarity 89.6%; Pred. No. 5.7e-94;
 Matches 543; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATCTTTGTTGAAAAAATGGAAAGACGTAGGACACACATGGACCTTGGTGCAACAAT 60
 Db 608 ATCTTTGTTGAAAAAATGGAAAGACGTAGGACACACATGGACCTTGGTGCAACAAT 549
 QY 61 ATTGTGTCCTCCAAATGTGTAACAAGGATTTTACATCTCTCCGGGTACTTTAAAGCTGAC 120
 Db 548 ATTGTGTCCTCCGAAAGTGTGTAACAAGGATTTTACATCTCTCCAGGTACCTTAAGTGAAC 489
 QY 121 TAGGACATTCACATTTATATTTGCGGTGCAATGAATTTGGTGCGCATTTCCCTCCACTTG 180
 Db 488 CAGGACATTCACATTTATATTTATCCCGTGCATGAATTTGGTGCGCATTTCCCTCCACTAG 429
 QY 181 GATTAGTCGGGGCGGAAAGTCAATCGGTATATTTAAATCCATCAATCAATGAAGAAATGTCACAGA 240
 Db 428 GATTGTTGGGCGAAAGTCAATCGGTATATTTAAATCCATCAATCAATGAAGAAATGTCACAGA 369
 QY 241 AATCTAAGTTGTAATGTTGCGAGCGTACTCGGTAGGGTGTGTTGGCGGTTTACCCC 300
 Db 368 AATCTAAGTTGTAATGTTGCGAGCGTACTCGGTAGGGTGTGTTGGTGGTTTGGCCCC 309
 QY 301 ACCCGGTGCTGAGGACACCAACATCAATCAGGTCATGCGACCTCTACACGAC 360
 Db 308 ACCCGGTGCTGAGGACACCAACATCAATCAGGTCATGCGACCTCTACACGAC 249
 QY 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCTAGTSCCCCTAGGCGCAT 420
 Db 248 CATCAAGTTGCAATTTAGTACGACCCCATATACGTGCGCATCTAGTSCCCCTAGGCGCAT 189
 QY 421 CAATGACCCAGGTTGGCTCGATCGAGAGCTGGGCCACCGCTATCGGGGTGATGCTG 480
 Db 188 TGATAACCCATGCTGGCTCGATCGAGAGCTGGGCCACCGCTATCGGGGTGATGCTG 129
 QY 481 CCCAGACGGTGTATGGACAGTTGTCGTACCTCGATAGTGGGACATAGTGAAGTCA 540
 Db 128 CCCAGACGGTGTATGGACAGTTGTCGTACCTCGATAGTGGGACATAGTGAAGTCA 69
 QY 541 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCCATGTTGTTGAAATTT 600
 Db 68 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCCATGTTGTTGAAACTAT 9
 QY 601 ATATGT 606
 Db 8 ATTTT 3

RESULT 2
 CK248798/c
 LOCUS
 DEFINITION EST732435 potato callus cDNA library, normalized and full-length
 Solanum tuberosum cDNA clone POCB364 5' end, mRNA sequence.

CK248798
 CK248798.1 GI:39799290
 EST.
 Solanum tuberosum (potato)
 Solanum tuberosum

KEYWORDS
 SOURCE
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE

AUTHORS

TITLE

JOURNAL

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asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 1004)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

Generation of ESTs from potato callus tissue

Unpublished (2003)

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1..1004

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="POCB364"

/tissue_type="callus"

/lab_host="DH10B-Tona"

/clone_lib="potato callus cDNA library, normalized and full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

Query Match 32.7%; Score 505.2; DB 14; Length 1004;

Best Local Similarity 89.6%; Pred. No. 5.5e-94;

Matches 543; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATCTTTGTTGAAAAAATGGAAAGACGTAGGACACACATGGACCTTGGTGCAACAAT 60

Db 607 ATCTTTGTTGAAAAAATGGAAAGACGTAGGACACACATGGACCTTGGTGCAACAAT 548

QY 61 ATTGTGTCCTCCAAATGTGTAACAAGGATTTTACATCTCTCCGGGTACTTTAAAGCTGAC 120

Db 547 ATTGTGTCCTCCGAAAGTGTGTAACAAGGATTTTACATCTCTCCAGGTACCTTAAGTGAAC 488

QY 121 TAGGACATTCACATTTATATTTGCGGTGCAATGAATTTGGTGCGCATTTCCCTCCACTTG 180

Db 487 CAGGACATTCACATTTATATTTAGCGGTGCAATGAATTTGGTGCGCATTTCCCTCCACTAG 428

QY 181 GATTAGTCGGGGCGGAAAGTCAATCGGTATATTTAAATCCATCAATGAAGAAATGTCACAGA 240

Db 427 GATTAGTCGGGGCGGAAAGTCAATCGGTATATTTAAATCCATCAATGAAGAAATGTCACAGA 368

QY 241 AATCTAAGTTGTAATGTTGCGAGCGTACTCGGTAGGGTGTGTTGGCGGTTTACCCC 300

Db 367 AATCTAAGTTGTAATGTTGCGAGCGTACTCGGTAGGGTGTGTTGGCGGTTTACCCC 308

QY 301 ACCCGGTGCTGAGGACACCAACATCAATCAGGTCATGCGACCTCTACACGAC 360

Db 307 ACCCGGTGCTGAGGACACCAACATCAATCAGGTCATGCGACCTCTACACGAC 248

QY 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCTAGTSCCCCTAGGCGCAT 420

Db 247 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCTAGTSCCCCTAGGCGCAT 188

QY 421 CAATGACCCAGGTTGGCTCGATCGAGAGCTGGGCCACCGCTATCGGGGTGATGCTG 480

Db 187 TGATAACCCATGCTGGCTCGATCGAGAGCTGGGCCACCGCTATCGGGGTGATGCTG 128

QY 481 CCCAGACGGTGTATGGACAGTTGTCGTACCTCGATAGTGGGACATAGTGAAGTCA 540

Db 127 CCCAGACGGTGTATGGACAGTTGTCGTACCTCGATAGTGGGACATAGTGAAGTCA 68

QY 541 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCCATGTTGTTGAAATTT 600

Db 67 CAAAGCAAGAGGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCCATGTTGTTGAAACTAT 8

QY 601 ATATGT 606

Db 8 ATTTT 3

Db	7	ATTTTT 2	
RESULT 3			
CK246326/c			
LOCUS	EST729963	potato callus cDNA library, normalized and full-length	EST 12-DEC-2003
DEFINITION	Solanum tuberosum cDNA clone POCAL08 5' end, mRNA sequence.		
ACCESSION	CK246326		
VERSION	CK246326.1	GI:39793747	
KEYWORDS	EST.		
SOURCE	Solanum tuberosum (potato)		
ORGANISM	Solanum tuberosum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.		
AUTHORS	Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.		
TITLE	Generation of ESTs from potato callus tissue		
JOURNAL	Unpublished (2003)		
COMMENT	Other ESTs: EST729964 Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org Clones can be requested from TIGR via potato@tigr.org Seq primer: ATT TAG GTG ACA CTA TAG.		
FEATURES	source	Location/Qualifiers	
		1..988	
		/organism="Solanum tuberosum"	
		/mol_type="mRNA"	
		/cultivar="Kennebec"	
		/db_xref="taxon:4113"	
		/clone="POCAL08"	
		/tissue_type="callus"	
		/lab_host="DH10B-Tona"	
		/clone_lib="potato callus cDNA library, normalized and full-length"	
		/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."	
ORIGIN			
	Query Match	32.5%	Score 502; DB 14; Length 988;
	Best Local Similarity	90.0%	Pred. No. 2.5e-93;
	Matches 538; Conservative	0; Mismatches 60; Indels 0; Gaps 0;	
Qy	1	ATCTTTGTTTGAATAAATTTGGAAGAACGTAGGACCATGGACCTTTGGTGCAACAAT	60
Db	598	ATCTTTGTTTGAATAAATCTAGACAAATCAGTAGGACCATGGACCTTTGGTGCAACAAT	539
Qy	61	ATTGTTGCTCTCCAAATGTTGACAGGATGTTACATCTCTCCGGTACTTTAAGCTGAC	120
Db	538	ATTGTTGCTCTCCGACGCTGGTACAGGATTTTACATCTCTCCAGGTACCTTAAGTGAAC	479
Qy	121	TAGGACATTCACCAATTTATTTGCGGTGCATTTGAATTCGCTGGCATTTCCCTCCACTTG	180
Db	478	CAGGACATTCACCAATTTATTTAGCGTGCATTTGAATTCGCTGGCATTTCCCTCCACTAG	419
Qy	181	GATTAGTCGGGGCGAAGTCATCGGTATATTAAATCCATCACTAAAGAAATGTCCGAGA	240
Db	418	GATTGTTGGGGCGAAGTCATCGGTATATTAAATCCATCACTAAAGAAATGTCCGAGA	359
Qy	241	AATCTAAGTTGTTGAACCTGGTCCGAGGCGTACTTCGGCTAGGCTGTTTGGCGGTTTACCCC	300
Db	358	AATCTAGTTTGTCTGAACCTGGTCCGAGGCGTATTTCAGCAGGGTGTGTTGGTGGTGGCCC	299
Qy	301	ACCCGGTGCACCTGCAGGACACCAACAATCACTACAGTCAATGACCAAGCTTCTACAGCAC	360
Db	298	ACCCGGTGCACCTGCAGGACACCAACAATCACTACAGTCTGCGCATGAACCTCTACAGCAC	239
Qy	361	CATCGAAGTTAGTCAGTACGACCCCATATACGTCGCATCTAGTCCGCTTAGGCGGCAT	420

Db	238	CATCAAGGTTGCAATTAGTACGACCCCATATACGTGCCACTTTAGTGCCTCGCGCAT	179
RESULT 4			
CK278032/c			
LOCUS	EST724110	potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAE351 5' end, mRNA sequence.	EST 12-DEC-2003
DEFINITION	Solanum tuberosum (potato)		
ACCESSION	CK278032		
VERSION	CK278032.1	GI:39835010	
KEYWORDS	EST.		
SOURCE	Solanum tuberosum (potato)		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.		
REFERENCE	1 (bases 1 to 888) Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B. Generation of ESTs from abiotic stressed potato tissue Unpublished (2003) Other ESTs: EST724111 Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org Clones can be requested from TIGR via potato@tigr.org Seq primer: ATT TAG GTG ACA CTA TAG.		
FEATURES	Location/Qualifiers	source	
		1..888	
		/organism="Solanum tuberosum"	
		/mol_type="mRNA"	
		/cultivar="Kennebec"	
		/db_xref="taxon:4113"	
		/clone="POAE351"	
		/tissue_type="abiotic stress treated leaf and root tissue"	
		/lab_host="DH10B-Tona"	
		/clone_lib="potato abiotic stress cDNA library"	
		/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, 1d, 2d, and 4d; Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library RNA sample."	

ORIGIN

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Query Match      32.4%; Score 500.2; DB 14; Length 888;
Best Local Similarity 90.2%; Pred. No. 6.1e-93;
Matches 535; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 ATCTTTGTTGAAAAATTGAAAAGAACGTAGGACCACTGGACCTTGGTGCACAAT 60
DB 594 ATCTTTGTTGAAAAATTGAAAAGAACGTAGGACCACTGGACCTTGGTGCACAAT 535
QY 61 ATTGTTGCTCCCAATTTGTTACCAAGGATTTGTTACATCTCCGGGTACTTTAAGCTGAC 120
DB 534 ATTGTTGCTCCCAATTTGTTACCAAGGATTTGTTACATCTCCGGGTACTTTAAGCTGAC 475
QY 121 TAGGACATTCACATTTATATTGCGCGGCAATGGAATGCGTGCATTTCCCTCCACTTG 180
DB 474 TAGGACATTCACATTTATATTGCGCGGCAATGGAATGCGTGCATTTCCCTCCACTTG 415
QY 181 GATTAGTCGGGGCGAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGCCAGA 240
DB 414 GATTAGTCGGGGCGAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGCCAGA 355
QY 241 AATCTAAGTTGTTGAACCTGCTCCGAGGCGTACTCGGCTAGGCTGTTTGGCGGTTTACCCC 300
DB 354 AATCTAAGTTGTTGAACCTGCTCCGAGGCGTACTCGGCTAGGCTGTTTGGCGGTTTACCCC 295
QY 301 ACCCGGTGCATCGCAGGACACCCACCAATCACCAGTCAATCAGCAACCTCTACGAGCAC 360
DB 294 ACCCGGTGCATCGCAGGACACCCACCAATCACCAGTCAATCAGCAACCTCTACGAGCAC 235
QY 361 CATCAAGTTACATCCAGTACGACCCCATATACGTCGCTAGTGCCTTCCCTAGCCGAT 420
DB 234 CATCAAGTTACATCCAGTACGACCCCATATACGTCGCTAGTGCCTTCCCTAGCCGAT 175
QY 421 CAATGACCCCAAGTTTGGCTCGATCGAGACGCTCGGCCACCCGCTATCGGGGTGATGCTG 480
DB 174 TGATTAACCCATGTCCTGGCTCGATCGAGACGCTCGGCCACCCGCTATCGGGGTGATGCTG 115
QY 481 CCCAGACGGTGTATGACAGAGTTTGTGCTACTCTGATGTGGGAGCATTAAGTGAAGTCA 540
DB 114 CCCAGACGGTGTATGACAGAGTTTGTGCTACTCTGATGTGGGAGCATTAAGTGAAGTCA 55
QY 541 CAAAAGCAAGGAGGAGAAAAACAAAAGAGATCTCAAGTAGCCCATGTTTGTG 594
DB 54 CAAAAGCAAGGAGGAGAAAAACAAAAGAGATCTCAAGTAGCCCATGTTTGTG 594

ORIGIN
Query Match      32.3%; Score 499.6; DB 14; Length 853;
Best Local Similarity 90.1%; Pred. No. 8.1e-93;
Matches 535; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATCTTTGTTGAAAAATTGAAAAGAACGTAGGACCACTGGACCTTGGTGCACAAT 60
DB 594 ATCTTTGTTGAAAAATTGAAAAGAACGTAGGACCACTGGACCTTGGTGCACAAT 535
QY 61 ATTGTTGCTCCCAATTTGTTACCAAGGATTTGTTACATCTCCGGGTACTTTAAGCTGAC 120
DB 534 ATTGTTGCTCCCAATTTGTTACCAAGGATTTGTTACATCTCCGGGTACTTTAAGCTGAC 475
QY 121 TAGGACATTCACATTTATATTGCGCGGCAATGGAATGCGTGCATTTCCCTCCACTTG 180
DB 474 TAGGACATTCACATTTATATTGCGCGGCAATGGAATGCGTGCATTTCCCTCCACTTG 415
QY 181 GATTAGTCGGGGCGAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGCCAGA 240
DB 414 GATTAGTCGGGGCGAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGCCAGA 355
QY 241 AATCTAAGTTGTTGAACCTGCTCCGAGGCGTACTCGGCTAGGCTGTTTGGCGGTTTACCCC 300
DB 354 AATCTAAGTTGTTGAACCTGCTCCGAGGCGTACTCGGCTAGGCTGTTTGGCGGTTTACCCC 295
QY 301 ACCCGGTGCATCGCAGGACACCCACCAATCACCAGTCAATCAGCAACCTCTACGAGCAC 360
DB 294 ACCCGGTGCATCGCAGGACACCCACCAATCACCAGTCAATCAGCAACCTCTACGAGCAC 235
QY 361 CATCAAGTTACATCCAGTACGACCCCATATACGTCGCTAGTGCCTTCCCTAGCCGAT 420
DB 234 CATCAAGTTACATCCAGTACGACCCCATATACGTCGCTAGTGCCTTCCCTAGCCGAT 175
QY 421 CAATGACCCCAAGTTTGGCTCGATCGAGACGCTCGGCCACCCGCTATCGGGGTGATGCTG 480
DB 174 TGATTAACCCATGTCCTGGCTCGATCGAGACGCTCGGCCACCCGCTATCGGGGTGATGCTG 115
QY 481 CCCAGACGGTGTATGACAGAGTTTGTGCTACTCTGATGTGGGAGCATTAAGTGAAGTCA 540
DB 114 CCCAGACGGTGTATGACAGAGTTTGTGCTACTCTGATGTGGGAGCATTAAGTGAAGTCA 55
QY 541 CAAAAGCAAGGAGGAGAAAAACAAAAGAGATCTCAAGTAGCCCATGTTTGTG 594
DB 54 CAAAAGCAAGGAGGAGAAAAACAAAAGAGATCTCAAGTAGCCCATGTTTGTG 594

RESULT 5
LOCUS CK271811/c
DEFINITION ES717889 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAD143 5' end, mRNA sequence.
ACCESSION CK271811
VERSION 1
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 853)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTs from abiotic stressed potato tissue
Other ESTs: ES717890
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1..853
/organism="Solanum tuberosum"

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Db	233	CATCAAGTTGCAATTTAGTACGCCCATATAGTGTCCATCTTAGTGCCCTCGGGGCAT	174
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Db	173	TGATACCCCATGCTGTGGCCCTCGATCGAGACGTCGGCCACCGCTATCGGGGTGATGCCG	114
QY	481	CCGACGCGTGTATGACACAGTTGTTCCGTACCTCGATAGTGGCAGCATATAGTGAAGTCA	540
Db	113	CCACACGCGTGTATGACACAGTTATTCGTCACCTCGATAGTGGCAGCATATAGTGAAGTCA	54
QY	541	CAAAAGCAAGAGGAGGAGAAAAAACAAGAAAGATCTCAAGTAGGCCATGTTTGT	592
Db	53	CAAAACCAAGGAGGAGAGAAAAACAAGAAAGATCTCAAGTAGGCCATGTTTGT	2
RESULT 7			
LOCUS	Bi176339/c		
DEFINITION	EST521129 P. infestans-challenged potato leaf, compatible reaction		
ACCESSION	Solanum tuberosum cDNA clone PPCAC11.5', sequence similar to		
VERSION	osmotin-like protein (Capsicum annuum), mRNA sequence.		
SOURCE	Bi176339		
KEYWORDS	Bi176339.1	GI:14642150	
ORGANISM	EST.		
REFERENCE	Solanum tuberosum (potato)		
AUTHORS	Solanum tuberosum		
TITLE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.		
JOURNAL	1 (bases 1 to 739)		
COMMENT	Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemiango, A., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E. and Baker, B. Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction Unpublished (2000)		
FEATURES	Contact: Robin Buell		
source	The Institute for Genomic Research		
	9712 Medical Center Dr, Rockville, MD 20850, USA		
	Email: potato-array@igr.org		
	This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:		
	http://genome.arizona.edu/orders/		
	Seq primer: M13P-R.		
	Location/Qualifiers		
	1..739		
	/organism="Solanum tuberosum"		
	/mol_type="mRNA"		
	/cultivar="Kennebec"		
	/db_xref="taxon:4113"		
	/clone="PPCAC11"		
	/tissue_type="leaf"		
	/dev_stage="6 week old"		
	/lab_host="SOLa"		
	/clone_lib="P. infestans-challenged potato leaf,		
	compatible reaction"		
	/note="Vector: pBluescript SX(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University, Fry lab; sequencing: The Institute for Genomic Research; whole plants were challenged with 20,000 sporangia/ml of the compatible P. infestans isolate US 940480. Leaf tissue was collected at 3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed first symptoms of infection at 48 hours after inoculation. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."		

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QY 1 ATCTTTGTTGAAAAAATTGGAAGAAGACGTAGGACCACATGGACCTTGGGTGCAACAAT 60
Db 587 ATCTTTGTTGAAAAAATCTCGACAAATCAGTAGGACCACATGGACCTTGGGTGCAACAAT 528
QY 61 ATTGTTGCTCCCAATATGGTACAGGATTTGATCATCTCCGGGTACTTTAAGCTGAC 120
Db 527 ATTGTTGCTCCCGAAGCTGGTACAGGATTTGATCATCTCCGGGTACTTTAAGCTGAC 468
QY 121 TAGGACATTCACCATTTATATTTGGCGTGCATGAATTCGCTGAGCTTTCCCTCCACTTG 180
Db 467 CAGGACATTCACCATTTATATGACCGTGCATGAATTCGCTGAGCTTTCCCTCCACTAG 408
QY 181 GATTAGTCGGGGCGAAGTCTATCGGTATATTAATTCATCAATCAATCAATCAATCAATCAAT 240
Db 407 GATTAGTCGGGGCGAAGTCTATCGGTATATTAATTCATCAATCAATCAATCAATCAATCAAT 348
QY 241 AATCTAAGTGTGTAAGTGTGCGAGGCTACTCGGCTAGGCTGTTTGGGGGTTTACCCC 300
Db 347 AATCTAAGTGTGTAAGTGTGCGAGGCTACTCGGCTAGGCTGTTTGGGGGTTTACCCC 288
QY 301 ACCCGTGCATCGCAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
Db 287 ACCCGTGCATCGCAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 228
QY 361 CATCGAAGTTACATCCAGTACAGCCCATATACGTGCGCATCGTAGTGGCCCTAGGCGCAT 420
Db 227 CATCAAGTTACATCCAGTACAGCCCATATACGTGCGCATCGTAGTGGCCCTAGGCGCAT 168
QY 421 CAATGACCCAGCTTTGGCTCGATCGAGACGTGCGCCACCCCTATCGGGTTCGATCGTG 480
Db 167 TGATGACCCAGCTTTGGCTCGATCGAGACGTGCGCCACCCCTATCGGGTTCGATCGTG 108
QY 481 CCCAGACGGTGTATGGAAGTGTGCTGCTACCTCGATAGTGGGAGCATTAAGTGAAGTCA 540
Db 107 CCCAGACGGTGTATGGAAGTGTGCTGCTACCTCGATAGTGGGAGCATTAAGTGAAGTCA 48
QY 541 CAAAGACGAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATG 587
Db 47 CAAAGACGAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATG 1

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RESULT 8
AW039873/c 649 bp mRNA linear EST 18-MAY-2001
LOCUS EST282346 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA
DEFINITION clone cLET13J13, mRNA sequence.
ACCESSION AW039873
VERSION AW039873.1 GI:5898627
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
ascidids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 649)
D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,
Fraser,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W.,
Rönnberg,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and
Giovannoni,J.
Generation of ESTs from tomato leaf tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..649
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"

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QY 1 ATCTTTGTTGAAAAAATTGGAAGAAGACGTAGGACCACATGGACCTTGGGTGCAACAAT 60
Db 587 ATCTTTGTTGAAAAAATCTCGACAAATCAGTAGGACCACATGGACCTTGGGTGCAACAAT 528
QY 61 ATTGTTGCTCCCAATATGGTACAGGATTTGATCATCTCCGGGTACTTTAAGCTGAC 120
Db 527 ATTGTTGCTCCCGAAGCTGGTACAGGATTTGATCATCTCCGGGTACTTTAAGCTGAC 468
QY 121 TAGGACATTCACCATTTATATTTGGCGTGCATGAATTCGCTGAGCTTTCCCTCCACTTG 180
Db 467 CAGGACATTCACCATTTATATGACCGTGCATGAATTCGCTGAGCTTTCCCTCCACTAG 408
QY 181 GATTAGTCGGGGCGAAGTCTATCGGTATATTAATTCATCAATCAATCAATCAATCAAT 240
Db 407 GATTAGTCGGGGCGAAGTCTATCGGTATATTAATTCATCAATCAATCAATCAATCAAT 348
QY 241 AATCTAAGTGTGTAAGTGTGCGAGGCTACTCGGCTAGGCTGTTTGGGGGTTTACCCC 300
Db 347 AATCTAAGTGTGTAAGTGTGCGAGGCTACTCGGCTAGGCTGTTTGGGGGTTTACCCC 288
QY 301 ACCCGTGCATCGCAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
Db 287 ACCCGTGCATCGCAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 228
QY 361 CATCGAAGTTACATCCAGTACAGCCCATATACGTGCGCATCGTAGTGGCCCTAGGCGCAT 420
Db 227 CATCAAGTTACATCCAGTACAGCCCATATACGTGCGCATCGTAGTGGCCCTAGGCGCAT 168
QY 421 CAATGACCCAGCTTTGGCTCGATCGAGACGTGCGCCACCCCTATCGGGTTCGATCGTG 480
Db 167 TGATGACCCAGCTTTGGCTCGATCGAGACGTGCGCCACCCCTATCGGGTTCGATCGTG 108
QY 481 CCCAGACGGTGTATGGAAGTGTGCTGCTACCTCGATAGTGGGAGCATTAAGTGAAGTCA 540
Db 107 CCCAGACGGTGTATGGAAGTGTGCTGCTACCTCGATAGTGGGAGCATTAAGTGAAGTCA 48
QY 541 CAAAGACGAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATG 587
Db 47 CAAAGACGAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATG 1

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RESULT 9
BI432833/c 583 bp mRNA linear EST 30-APR-2003
LOCUS EST535594 P. infestans-challenged potato leaf, compatible reaction
DEFINITION Solanum tuberosum cDNA clone PPCAW35 5' sequence, mRNA sequence.
ACCESSION BI432833
VERSION BI432833.1 GI:15257523
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
ascidids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 583)
Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,

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/clone="cLET13J13"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF,"
/clone_lib="tomato mixed elicitor, BTI"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XbaI; CLET - Incubated with a variety of disease response
elicitors. Plants exposed to 2,6 dichloroisocotinic
acid, BTH, jasmonic acid, ethylene, fenthion, EIX,
okadaic acid, or systemin prior to tissue harvest. EcoRI
site was destroyed during cloning."

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ORIGIN

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Query Match 31.7%; Score 490.2; DB 9; Length 649;
Best Local Similarity 89.3%; Pred. No. 7.4e-91;
Matches 528; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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```

QY 1 ATCTTTGTTGAAAAAATTGGAAGAAGACGTAGGACCACATGGACCTTGGGTGCAACAAT 60
Db 587 ATCTTTGTTGAAAAAATCTCGACAAATCAGTAGGACCACATGGACCTTGGGTGCAACAAT 528
QY 61 ATTGTTGCTCCCAATATGGTACAGGATTTGATCATCTCCGGGTACTTTAAGCTGAC 120
Db 527 ATTGTTGCTCCCGAAGCTGGTACAGGATTTGATCATCTCCGGGTACTTTAAGCTGAC 468
QY 121 TAGGACATTCACCATTTATATTTGGCGTGCATGAATTCGCTGAGCTTTCCCTCCACTTG 180
Db 467 CAGGACATTCACCATTTATATGACCGTGCATGAATTCGCTGAGCTTTCCCTCCACTAG 412
QY 181 GATTAGTCGGGGCGAAGTCTATCGGTATATTAATTCATCAATCAATCAATCAATCAAT 240
Db 407 GATTAGTCGGGGCGAAGTCTATCGGTATATTAATTCATCAATCAATCAATCAATCAAT 352
QY 241 AATCTAAGTGTGTAAGTGTGCGAGGCTACTCGGCTAGGCTGTTTGGGGGTTTACCCC 300
Db 347 AATCTAAGTGTGTAAGTGTGCGAGGCTACTCGGCTAGGCTGTTTGGGGGTTTACCCC 292
QY 301 ACCCGTGCATCGCAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
Db 287 ACCCGTGCATCGCAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 232
QY 361 CATCGAAGTTACATCCAGTACAGCCCATATACGTGCGCATCGTAGTGGCCCTAGGCGCAT 420
Db 231 CATCAAGTTACATCCAGTACAGCCCATATACGTGCGCATCGTAGTGGCCCTAGGCGCAT 172
QY 421 CAATGACCCAGCTTTGGCTCGATCGAGACGTGCGCCACCCCTATCGGGTTCGATCGTG 480
Db 171 TGATGACCCAGCTTTGGCTCGATCGAGACGTGCGCCACCCCTATCGGGTTCGAGCGCG 112
QY 481 CCCAGACGGTGTATGGAAGTGTGCTGCTACCTCGATAGTGGGAGCATTAAGTGAAGTCA 540
Db 111 CCCAGACGGTGTATGGAAGTGTGCTGCTACCTCGATAGTGGGAGCATTAAGTGAAGTCA 52
QY 541 CAAAGACGAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATGTTT 591
Db 51 CAAAGACGAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATGTTT 1

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RESULT 9
BI432833/c 583 bp mRNA linear EST 30-APR-2003
LOCUS EST535594 P. infestans-challenged potato leaf, compatible reaction
DEFINITION Solanum tuberosum cDNA clone PPCAW35 5' sequence, mRNA sequence.
ACCESSION BI432833
VERSION BI432833.1 GI:15257523
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
ascidids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 583)
Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,

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Bougri, O., Buell, C.R., Roming, C.M., Fry, W.E. and Baker, B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, Compatible Interaction
Unpublished (2000)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.

FEATURES

source
1. .583
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PPCW35"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/clone_lib="P. infestans-challenged potato leaf,
compatible reaction"
/note="Vector: pBluescript SK(-); Site_1: EcoRI, Site_2:
XhoI, supplier: Cornell University, Fry lab; sequencing:
The Institute for Genomic Research; Whole plants were
challenged with 20,000 sporangia/ml of the compatible P.
infestans isolate US 940480. Leaf tissue was collected at
3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen
in liquid nitrogen immediately upon removal. Kennebec
plants showed first symptoms of infection at 48 hours
after inoculation. NOTE: We cannot exclude the
possibility that this sequence is actually derived from
Phytophthora rather than potato."

ORIGIN

Query Match 31.5%; Score 487.2; DB 12; Length 583;
Best Local Similarity 90.0%; Pred. No. 3.1e-90;
Matches 522; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 19 TGGAAAGAAAGTAGGACACATGACCTGGGTGCAACAATATTGTTGCTCTCAATG 78
DB 581 TCGACAAATCAGTAGGACACATGACCTGGGTGCAACAATATTGTTGCTCTCGRACG 522

QY 79 TGGTACAGGATTGTATCATCTCCGGTACTTTAACTGACTAGGACATTCACATTTA 138
DB 521 TGGTACAGGATTGTATCATCTCCAGTACCTTAAGTGAACCCAGGACATTCACATTTA 462

QY 139 TATTTGCCGTGATTAATTTGGTGGCATTTCCCTCCACTTGGATTAGTCGGGGCGAAAG 198
DB 461 TATTAGCGTGCAATGAATTTGGTGACATTTCCCTCCACTAGGATTGTTGGGGCGAAAG 402

QY 199 TCATCGGTATTAATCAATCACTAAGAAATGTCAGAAATCTAAGTTGTGAAT 258
DB 401 TCATCGGAATATTAATCAATCATCGACTAAGAAATGTCAGAAATCTAGTTGTGTAAT 342

QY 259 GGTCCGAGCGTACCTGCGGTAGGTGTTGGGGTTTACCCACCCGCGTACATGCGAGA 318
DB 341 GGTCCAGCGGTACTCGGTAGGTGTTGGGGTTTACCCACCCGGTACATTTGCGAGA 282

QY 319 CACCAACCAATCACCGATGACGAACTTACACGACCATTCGAAAGTTACATCCAG 378
DB 281 CCCCACCAATCACCGATGATGAACTTCTCCAGCACCACCAAGTTACATTTAG 222

QY 379 TACGACCCATATAGTCCGATCTAGTCCGCTAGGCGATCAATGACCCACCTTTGGC 438
DB 221 TACGACCCATATAGTCCGATCTTTAGTACCCCTCGGCGCATTTGATGACCATCTGCGC 162

QY 439 CTCGATCGAGACGTCCGCGACCGCTATCGGGTTCGATGCTGCCACACGGTGTATGAC 498
DB 161 CTCGATCGAGACGTCCGCGACCGCTATCGGGTTCGATGCTGCCACACGGTGTATGAC 102

QY 499 AGTTGTTGCGTACCTCGATAGTGGCAGCATAGTGAAGTCAAAAAGCAAGAGGAGA 558
DB 101 AGTTGTTGCGTACCTCGATAGTGGCAGCATAGTGAAGTCAAAAAGCAAGAGGAGA 42

QY 559 AAACAAAAGAAGATCTCAAGTAGCCCATGTTTCTTGAAT 598
DB 41 AAACAAAAGAAGATCTCAAGTAGCCCATGTTTCTTGAAT 2

RESULT 10

BF053678/c
LOCUS

DEFINITION EST438908 potato leaves and petioles Solanum tuberosum cDNA clone
CSTB36B20 5' sequence, mRNA sequence.

ACCESSION BF053678

VERSION

KEYWORDS EST.

SOURCE

ORGANISM Solanum tuberosum (potato)

REFERENCE

AUTHORS van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Uterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R.,
Roming, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
Unpublished (2000)

COMMENT

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/.

FEATURES

source
1. .622

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="CSTB36B20"

/tissue_type="leaflets and petioles"

/dev_stage="8 weeks old plants"

/lab_host="SOLR"

/clone_lib="potato leaves and petioles"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Tissue was supplied by Dr. Fry (Cornell University).
Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."

ORIGIN

Query Match 31.4%; Score 486; DB 10; Length 622;
Best Local Similarity 89.0%; Pred. No. 5.5e-90;
Matches 525; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATCTTTGTTGAAAAAATTGAAAAAGACGTAGGACACATGACCTTGGTGCAACAAT 60
DB 599 ATCTTTGTTGAAAAAATCTCGACCATGCTAGGACACATGACCTTGGTGCAACAAT 540

QY 61 ATTGTTGTCTCTCCAAATGTTGGTCAAGGATTGTACATCTCCGGTACTTTAAGCTGAC 120
DB 539 ATTGTTGTCTCTGACGTTGGTACAGGATTGTACATCTCCGGTACTTTAAGTTGAC 480

QY 121 TAGGACATTCACATTTATTGTCGCGTGAATTGAATTCGTTGGCATTTCCCTCCACTTG 180
DB 479 CAGGGCATTCACCATTTATTGTCGCGTGAATTGAATTCGTTGGCATTTTCCTCCACTAG 420

QY 181 GATTAGTCGGGGGAAAGTCATCGGTATATTAATCCATCACTAAGAAATGTCCTCCAGA 240
DB 419 GATTGTCGGGGGAAAGTCATTTGTTATTAATCCGTAACCTAAGAAATGTCCTCCAGA 360

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241 AATCTAAGTTGTTGAACCTGGTCCGAGCGGTACTCGGTAGGTGTTTGGGGTTTACCCC 300
Db
359 AATCTAGGTTGTTAACTGATTCAAGGCATATTCCGCCAGGGTGTGGGGGTTTACCCC 300
QY
301 ACCGGTGCATCGAGGACACACCAATCACCAGTCATGCGAAGCTTACCCAGCAC 360
Db
299 ACCGGGTACATGCAAGACTCCACCAATCACCAGTCTGCAAGAACCTCTACCAGCAC 240
QY
361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCTTAGCGGCAT 420
Db
239 CATCAAGTTGCAATTAGTACGACCCCATATACGTGCGCATCTAGTCCCTCGGTGCAT 180
QY
421 CAATGACCCAGCTTTGGCGCTCGATCGAGACGTGCGGCACCGCCCTATCGGGGTGATGCTG 480
Db
179 TGATGACCCAAAGTTTGACCTCGATCGAGACGTGCGGCACCGCCCTATCGGGGTTGATGCG 120
QY
481 CCCAGACGCTGATGACAGCTGTTGCGTACTCGATAGTGGCAGCATAGTGAAGTCA 540
Db
119 CCCAGACGCTGATGACAGCTGTTGCGTACTCGATAGTGGCAGCATAGTGAAGTCA 60
QY
541 CAAAAGCAAGGAGGAGAAAAAAGAAAGATCTCAAGTAGCCCATGTTT 590
Db
59 CAAAAGCAAGGAGGAGAAAAAAGAAAGATCTCAAGTAGCCCATGTTT 10

RESULT 11
BG130690/c
LOCUS
DEFINITION
  BG130690 639 bp mRNA linear EST 31-JAN-2001
  EST463582 tomato crown gall Lycopersicon esculentum cDNA clone
  cTOE1A9 5' sequence similar to putative pathogenesis-related
  protein PR P23, mRNA sequence.
ACCESSION
  BG130690
KEYWORDS
  BG130690.1 GI:12630878
SOURCE
  Lycopersicon esculentum (tomato)
  Lycopersicon esculentum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE
  1 (bases 1 to 539)
  van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Hansen,C.,
  Ronning,C. and Tanksley,S.
  Generation of ESTs from tomato crown gall tissue
  Unpublished (2001)
  Contact: CUGI
  Clemson University Genomics Institute
  Clemson University
  100 Jordan Hall, Clemson, SC 29634, USA
  Email: http://www.genome.clemson.edu/orders/index.html.
  Location/Qualifiers
    1..639
    /organism="Lycopersicon esculentum"
    /mol_type="mRNA"
    /cultivar="TA496"
    /db_xref="taxon:4081"
    /clone="cTOE1A9"
    /tissue type="crown gall"
    /dev stage="crown galls from full-grown plants (8 wks
    old)"
    /lab host="SOLR"
    /clone_lib="tomato crown gall"
    /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
    XhoI; Four wk old greenhouse plants were stab inoculated
    on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr,
    Cornell U.). Galls were allowed to develop for another 4
    wks, when gall tissue was frozen in liquid nitrogen."

FEATURES
  source
    Query Match 31.4%; Score 485.2; DB 12; Length 639;
    Best Local Similarity 89.2%; Pred. No. 8e-90;
    Matches 523; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

ORIGIN

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QY
1 ATCTTTGTTGAAAAAATTTGAAAAAGAACGTAGGACCAATGGACCTTTGGGTGCAACAAT 60
Db
587 ATCTTTGTTGAAAAAATCTCGACAAATCAGTAGGGCCACATGGACCTTTGTGTGCAACAAT 528
QY
61 ATTGTTGCTCTCCAAATGTTGGTACAGGATTTTACATCTCTCCGGGTACTTTAAGCTCAC 120
Db
527 ATTGTTGCTCTCCGAACGTGGTACAGGATTTTACATCTCTCCGGGTACTTTAAGTGAAC 468
QY
121 TAGGACATTCACATTTATTTGCGGTGCAATTTGAATTTGCGTGGCAATTTCCCTCCACTTG 180
Db
467 CAGGACATTCACATTTATTTAGCCGTACAAATGAATTTGCATGGCAATTTCCCTCCACTTAG 408
QY
181 GATTAGTGGGGGGAAGTCATCGGTATATTAAATCCATCACTAAAGAAATGTCCCGAGA 240
Db
407 GATTAGTGGGGGGAAGTCAATTTGAATTTAAATCCATCACTAAAGAAATGTCCCGAGA 348
QY
241 AATCTAAGTTGTTGAACCTGGTCCGAGCGGTACTCGGGTAGGTGTTTGGCGGTTTACCCC 300
Db
347 AATCTAGGTTGCTAAACTGGTCCAAAGCGTACTCGGCCAGGGTGTGTTGGTGGTTGCCCC 288
QY
301 ACCCGTGCATGCGAGGACACCAACCAATCACCAGTCATGCGAAGCTTACCCAGCAC 360
Db
287 ACCCGGTACATTTGCAAGACCCGCCAACCAATCACCAGTCTGACATGAACCTCTACGAGCAC 228
QY
361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCTTAGCGGCAT 420
Db
227 CATCAAGTTGCAATTCGTACGACCCCATATACGTGCGCATCTTAGTGCCTCGGTGCAT 168
QY
421 CAATGACCCAGCTTTGGCGCTCGATCGAGACGTGCGGCCACCGCCCTATCGGGGTGCAATGCTG 480
Db
167 TGATGACCCCATTTTGGCGCTCGATCAAGACGTGCGACCAACCGCCCTATTGGGGTTCGACGCGC 108
QY
481 CCCAGACGCTGATGACAGCTGTTGCGTACTCGATAGTGGCAGCATAGTGAAGTCA 540
Db
107 CCCAGACGCTGATGACAGCTGTTGCGTACTCGATAGTGGCAGCATAGTGAAGTCA 48
QY
541 CAAAAGCAAGGAGGAGAAAAAAGAAAGATCTCAAGTAGCCCAT 586
Db
47 CAAAAGCAAGGAGGAGAAAAAAGAAAGATCTCAAGTAGGCCAT 2

RESULT 12
BG122472/c
LOCUS
DEFINITION
  BG122472 657 bp mRNA linear EST 17-OCT-2001
  EST542376 tomato callus Lycopersicon esculentum cDNA clone
  cLEC7J15 5' end, mRNA sequence.
ACCESSION
  BG122472
VERSION
  BG122472.1 GI:16219560
KEYWORDS
  EST.
SOURCE
  Lycopersicon esculentum (tomato)
  Lycopersicon esculentum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE
  1 (bases 1 to 657)
  Alcalá,J., Vrebalov,J., White,R., Vision,T., Karanycheva,S.A.,
  Tsai,J., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M.,
  Martin,G.B., Tanksley,S.D. and Giovannoni,J.
  Generation of ESTs from tomato callus tissue (2001)
  Unpublished (2001)
  Contact: CUGI
  Clemson University Genomics Institute
  Clemson University
  100 Jordan Hall, Clemson, SC 29634, USA
  Email: http://www.genome.clemson.edu/orders/index.html
  This clone is available through the Clemson University Genomics
  Institute
  Seq primer: T3
  Location/Qualifiers
    1..657
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    /mol_type="mRNA"
    /cultivar="TA496"

FEATURES
  source
    Query Match 31.4%; Score 485.2; DB 12; Length 639;
    Best Local Similarity 89.2%; Pred. No. 8e-90;
    Matches 523; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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/clone_lib="tomato callus"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Boyce Thompson Institute; sequencing: The
Institute for Genomic Research; cLEC - Cotyledons of
seedlings 7-10 days post-germination were excised, cut at
both ends and placed on MS medium with no selection. Mixed
callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST library"

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ORIGIN

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Query Match      31.2%; Score 483; DB 12; Length 567;
Best Local Similarity 88.2%; Pred. No. 2.3e-89;
Matches 525; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 4 TTTGTTGAAAAAATGGAAAGACGTAGGACCAACATGACCTTGGGTGCAACAATATT 63
DB TCTGTTGAAAAATCTCGACAAATCAGTAGGCGCACATGGACCTTGTGCAACATATT 537
QY 64 GTTGCTCTCAATGTGTACAGGATTGTTCATCTCCGGGTACTTTAAGTGTGACTAG 123
DB GTTGCTCTCCGAACGTGTGTACAGGATTGTTCATCTCCGGGTACTTTAAGTGTGACTAG 477
QY 124 GACATTCACCATTTATTTGCGGTGCTATGTAATTCGTTGGGTACTTTCCCTCCACTTGGAT 183
DB GACATTCACCATTTATTTAGCCGTACATGTAATTCGTTGGGTACTTTCCCTCCACTTGGAT 417
QY 184 TAGTCGGGGCGAAAGTCATCGGTATATTAATFCCAATCAACTAAAGAAATGTCCAGAAAT 243
DB TGGTCGGGGCGAAAGTCATCGGTATATTAATFCCAATCAACTAAAGAAATGTCCAGAAAT 357
QY 244 CTAAGTTGTGAACGTCCGAGGCGTACTCGCTAGGGTGTTCGGCGTTTACCCACC 303
DB CTAGGTGTCTAACTGGTCCAGGCGTACTCGGCGAGGGTGTTCGGTGTTCGGCGTTTACCCACC 297
QY 304 CGGTGCATCGAGGACACACCAATCACCAGTCAATGACGAACTCTACCGACCAAT 363
DB CGGTGCATCGAGGACACACCAATCACCAGTCAATGACGAACTCTACCGACCAAT 237
QY 364 CGAAGTTACATCCAGTAGACCCCATATAGTGCCATCGTGTGCGCCCTTAGCGGATCAA 423
DB CAAAGTTGCAATTCGTACGACCCCATATAGTGCCATCTTAGTGCCCTCGGTGCAATGA 177
QY 424 TGACCCAGCTTTGGCTCGATCGACGCTCGSCACCGCCTATCGGGTTCGATGCTGCC 483
DB TGACCCATGTTGGCTCGATCGACGCTCGACCCGCTATCGGGTTCGACCGCGCC 117
QY 484 AGACGGTGTATGACAGTGTGTGCGTACCTCGATAGTGGCAGCATAAAGTGAAGTCAAA 543
DB AGACGGTGTATGACAGTGTGTGCGTACCTCGAAGTGGCAGCATAAAGTGAAGTCAAA 57
QY 544 AGCAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAAT 598
DB AAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGGAAT 2

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RESULT 13
LOCUS AW031249/c
DEFINITION EST274624 tomato callus, TAMU Lycopersicon esculentum cDNA clone
cLEC34F24 similar to osmotin-like protein TPM-1 precursor (PR P23),
mRNA sequence.
ACCESSION AW031249
VERSION AW031249.1 GI:5889926
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 585)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
Giovannoni,J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..585
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC34F24"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRF"
/clone_lib="tomato callus, TAMU"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"

```

FEATURES

source

Query Match 31.1%; Score 480.8; DB 9; Length 585;
Best Local Similarity 89.0%; Pred. No. 6.6e-89;
Matches 518; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

ORIGIN

```

QY 19 TGGAAAGAGACGTAGGACCAACATGACCTTGGGTGCAACAATATTGTTCCTCCAAATG 78
DB TCACAAATCAGTAGGNCACATGGACCTTGTGCAACAATATTGTTCCTCCGACG 524
QY 79 TGTACAGGATTGTTCATCTCCGGTACTTTAAGCTGCTAGGACATTCACATTTA 138
DB TGTACAGGATTGTTCATCTCCGGTACTTTAAGCTGCTAGGACATTCACATTTA 454
QY 139 TATTGCGGTGCAATGCAATTTGGTGGCATTTCCCTCCACTTGGATTAGTCGGGCGGAAAG 198
DB TATTAGCCGTACATGCAATTTGGTGGCATTTCCCTCCACTTGGATTAGTCGGGCGGAAAG 404
QY 199 TCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCAGAAATCTAAGTTGTGAAT 258
DB TCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCAGAAATCTAAGTTGTGAAT 344
QY 259 GGTCCGAGGCTACTCGGTAGGTTGTTGGCGTTTACCCACCGGTGCTACGAGGA 318
DB GGTCCGAGGCTACTCGGTAGGTTGTTGGTGGTTTGGCCCGGACCGGTACATTCGAAGA 284
QY 319 CACACCACAATCACCAGTCAATCGACGAACTCTACAGCACCATCGAAGTTACATCCAG 378
DB CACACCACAATCACCAGTCTGACATGAACCTCTACAGCACCATCAAGTTGCAATTCG 224
QY 379 TAGACCCCATATACGTGCGCATGTAGTGCCTTAGCGCATCAATGACCCAGTTTGGC 438
DB TAGACCCCATATACGTGCGCATGTAGTGCCTTAGCGCATCAATGACCCAGTTTGGC 164
QY 439 CTCGATCGAGACGTCCGGCCACCGCCCTATCGGGTTCGATGTCGCCAGCGGTGTATGGAC 498
DB CTCGATCAAGACGTCCGACCCGCTATTTGGGGTTCGACCGCCCGCCAGCGGTGTATGGAC 104
QY 499 AGTTGTTGGTACTCTCGATGTGGGAGCATAAGTGAAGTCAAAAGCAAGAGGAGGA 558
DB AGTTGTTGGTACTCTCGAAGTGGGAGCATAAGTGAAGTCAAAAGCAAGAGGAGGA 44

```


/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Giovannoni laboratory;_cIEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"

ORIGIN		Query Match	30.7%;	Score 474.4;	DB 9;	Length 583;
		Best Local Similarity	88.6%;	Pred. No. 1.4e-87;		
		Matches 514;	Conservative 0;	Mismatches 66;	Indels 0;	Gaps 0;
QY	19	TGAAAAAGACGTAGGACACATGACCTTGGTGCAACAATATTGTTGTCTCTCAAAATG	78			
Db	581	TCGACAAATCAGTAGGGCCACATGACCTTGTGCAACAATATTGTTGTCTTCGGAACG	522			
QY	79	TGGTACAGGATTGTATCATCTCCGGGTACTTTAAGCTGACTAGGACATTCACCATTTA	138			
Db	521	TGGTACAGGATTGTATCATCTTCGGGTACCGTAAGTGAACCCAGGACATTCACCATTTA	462			
QY	139	TATTTGCGGTGCATTGAATTGCGTGGCATTTCCCTCCACTTCGATTAGTCGGGGCGAAAG	198			
Db	461	TATTAGCGGTACAATGAATTGCATGGCATTTCCCTCCACTAGGATTGTCGGGGCGAAAG	402			
QY	199	TCAATCGGTATTATAATCAATCACTAAAGAAATGTCCAGAAATCTAAGTTGTGAACT	258			
Db	401	TCATTGGAATATTAAATCCATCGACTAAAGAAATGTCCAGAAATCTAGGTTGCTAAACT	342			
QY	259	GGTCCGAGCGTACTCGGTAGGGTGTGTTGGGGTTTACCCACCCGGTGCACTGCAGGA	318			
Db	341	GGTCCAGGCGTACTCGGCCAGGGTGTGTTGGTGTTCGCCACCCGGTACATTGCCAGA	282			
QY	319	CACCAACCAATCACCAGTCAATGCAAGAACTCTACAGCACCATCGAAGTTACATCCAG	378			
Db	281	CCCCACCAATCACCAGTCTGACATGAACCTCTACCAGCACCATCAAGTTGCAATTCG	222			
QY	379	TACGACCCCATATAGTGCCATCGTAGTGCCCTAGCGGCATCAATGACCCACGTTTGGC	438			
Db	221	TACGACCCCATATAGTGCCATCTTTAGTGCCCCCTCGGTGCAATTGATGCCCATGTTTGGC	162			
QY	439	CTCGATCGAGACGTCCGGCCACCGCCTATCGGGGTGATGCTGCCCCAGACGGGTATGGAC	498			
Db	161	CTCGATCAAGAGCTCGACCCACCGCCTATTGGGGTCGACCGCCCGACGCGTGTATGGAC	102			
QY	499	AGTTGTTGCGTACCTCGATAGTGGCAGCATTAAGTGAAGTCAAAAGCAAGAAGGGAGA	558			
Db	101	AGTTGTTGCGTACCTCGAAGTGGCAGCATTAAGTGAAGTCAAAAGCAAGAAGGGAGA	42			
QY	559	AAACAAAAGAGATCTCAAGTAGCCCATGTTTGTGAAAT	598			
Db	41	AAACAAAGAGAGATCTCAAGTAGGCCCATGTTTGTGAACT	2			

Search completed: August 18, 2004, 16:04:26
Job time : 3636.85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 03:32:09 ; Search time 552.632 Seconds
(without alignments)
11884.422 Million cell updates/sec

Title: US-10-051-307-3
Perfect score: 1546
Sequence: 1 atctctgttgaaaaaattg.....tggtgaagttggtgtttc 1546

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002s.*
7: geneseqn2003as.*
8: geneseqn2003bs.*
9: geneseqn2003cs.*
10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1532.2	99.1	1546	6	Abk90562 Potato pr
2	1362.4	88.1	1595	6	Abk90560 Potato pr
3	1334.4	86.3	1598	6	Abk90561 Potato pr
4	500	32.3	3033	2	Aav52754 Nicotiana
5	500	32.3	3033	2	Aax16340 Tobacco o
6	450.4	29.1	883	2	Aaq15269 Osmotin-1
7	450.4	29.1	884	2	Aaq15270 Encodes C
8	448.4	29.0	741	2	Aav68641 Nucleotid
9	382.2	24.7	1004	2	Aaq21414 Encodes o
10	288.2	13.5	906	3	Aac47993 Arabidops
11	207.8	13.4	902	3	Aac47227 Arabidops
12	207.2	13.4	735	6	Abz14313 Arabidops
13	207.2	13.4	735	7	Abz42096 Arabidops
14	207.2	13.4	735	7	Ada68525 Arabidops
15	207.2	13.4	950	6	Abn98566 Arabidops
16	180.6	11.7	875	5	Aac84839 Sunflower
17	172.4	11.2	771	3	Aaz23511 Asparagus
18	159.2	10.3	900	1	Aan90842 Fragment
19	159.2	10.3	900	2	Aav62808 Tobacco p
20	159.2	10.3	900	2	Aav72992 PR-R majo
21	153.8	9.9	549	3	Aac5150 Arabidops
22	152.6	9.9	910	4	Aad04241 Sunflower
23	143.8	9.3	2000	7	Ada71704 Rice gene

C 24	132.4	8.6	500	3	AAA40422
C 25	128.4	8.3	693	2	AAQ58991
C 26	127.4	8.2	627	2	AAQ58932
C 27	124.8	8.1	894	2	AAQ91491
C 28	116.2	7.5	705	1	AAAN40215
C 29	115.4	7.5	343	6	ABQ85936
C 30	112	7.2	1932	7	ADA71064
C 31	109.4	7.1	950	2	AAQ06184
C 32	109.4	7.1	1970	7	ADA71063
C 33	104.4	6.8	808	2	AAV28688
C 34	102.4	6.6	669	7	ADA59630
C 35	101	6.5	1309	2	AAQ4913
C 36	101	6.5	1309	2	AAQ4914
C 37	95.6	6.2	621	1	AAAN70934
C 38	94.4	6.1	621	6	ABQ78707
C 39	94.4	6.1	621	9	AAQ59196
C 40	94	6.1	621	1	AAAN70933
C 41	94	6.1	621	6	ABQ78703
C 42	94	6.1	621	9	AAQ59192
C 43	94	6.1	639	1	AAAN50328
C 44	82	5.3	961	1	AAAN20003
C 45	81.4	5.3	624	2	AAAT06312

ALIGNMENTS

RESULT 1
ABK90562
ID ABK90562 standard; DNA; 1546 BP.
XX
AC ABK90562;
XX
DT 15-NOV-2002 (first entry)
XX
DE Potato proteinase inhibitor 1 (pinl) gene promoter isoform III.
XX
KW Potato; proteinase inhibitor 1; pinl; promoter; ds; plant;
KW Controlled Environmental Agriculture; crop cultivation.
XX
OS Solanum tuberosum.
XX
PN WO200259333-A2.
XX
PD 01-AUG-2002.
XX
PF 18-JAN-2002; 2002WO-US001287.
XX
PR 23-JAN-2001; 2001US-0263224P.
XX
PA (DAIZ/) DAI Z.
PA (SHIL/) SHI L.
PA (HOOK/) HOOKER B S.
XX
Dai Z, Shi L, Hooker BS;
WPI; 2002-608457/65.
XX
PT New proteinase inhibitor 1 (pinl) or aminotransferase (amt) gene promoter
PT isoforms derived from potato, useful in manipulating expression of genes
PT and in Controlled Environmental Agriculture for heterologous protein
production.
XX
PS Claim 2; Fig 3; 43pp; English.
XX
CC The invention relates to polynucleotides having proteinase inhibitor 1
CC (pinl) or aminotransferase (amt) gene promoter activity. Isoforms of pinl
CC and amt gene promoters are useful in manipulating expression of genes,
CC particularly in transformed plant cells. The gene promoters are useful in
CC constructing gene expression vectors and in Controlled Environmental
CC Agriculture for heterologous protein production. The vectors are useful
CC in facilitating the expression and/or secretion of heterologous proteins
CC in cell culture or by crop cultivation. The new gene promoter isoforms

CC provide high level, stable and controllable expression that is
 CC temporarily, environmentally, or developmentally regulatable. This
 CC sequence represents a potato pin1 gene promoter isoform

XX
 SQ Sequence 1546 BP; 501 A; 270 C; 284 G; 490 T; 0 U; 1 Other;

Query Match	99.1%;	Score 1532.2;	DB 6;	Length 1546;
Best Local Similarity	99.5%;	Pred. No. 0;		
Matches 1538;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
QY	1	ATCTTTGTTTCAAAAATGGAAGAAGCGTAGGACACATGACCTTGGTGCAACAAT	60	
DB	1	ATCTTTGTTTCAAAAATGGAAGAAGCGTAGGACACATGACCTTGGTGCAACAAT	60	
QY	61	ATTCTTGTCTCCAAATGTGGTCAAGGATGTTPACATCTCCGGGACTTTAAGCTGAC	120	
DB	61	ATTCTTGTCTCCAAATGTGGTCAAGGATGTTPACATCTCCGGGACTTTAAGCTGAC	120	
QY	121	TAGACATTCACATTTATATTTCCGTCGATTCGAATTCGTCGATTTCCCTCCACTTG	180	
DB	121	TAGACATTCACATTTATATTTCCGTCGATTCGAATTCGTCGATTTCCCTCCACTTG	180	
QY	181	GATTAGTCGGGGGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCACAG	240	
DB	181	GATTAGTCGGGGGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCACAG	240	
QY	241	AATCTAAGTTTGGAACTGGTCCGAGCGTACTCGGCTAGGGTGTGGGGTTTACCCC	300	
DB	241	AATCTAAGTTTGGAACTGGTCCGAGCGTACTCGGCTAGGGTGTGGGGTTTACCCC	300	
QY	301	ACCGGTGCTACTGAGGACACCAACAATCACCAGTCATGCACGAACCTCTACACGAC	360	
DB	301	ACCGGTGCTACTGAGGACACCAACAATCACCAGTCATGCACGAACCTCTACACGAC	360	
QY	361	CATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCTGATGCCCTTAGGGCAT	420	
DB	361	CATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCTGATGCCCTTAGGGCAT	420	
QY	421	CAATGACCCAGCTTGGCTCGATCGAGAGCTGGCCACCGCTATCGGGGTGATGCTG	480	
DB	421	CAATGACCCAGCTTGGCTCGATCGAGAGCTGGCCACCGCTATCGGGGTGATGCTG	480	
QY	481	CCCAGACGGTGTAGGACAGTTGTTGGCTACCTCGATAGTGGCAGCATAAAGTCA	540	
DB	481	CCCAGACGGTGTAGGACAGTTGTTGGCTACCTCGATAGTGGCAGCATAAAGTCA	540	
QY	541	CAAAAGCAGAGGAGGAGAAACAAGAAGATCTCAAGTAGCCCATGTTGTTGAATTT	600	
DB	541	CAAAAGCAGAGGAGGAGAAACAAGAAGATCTCAAGTAGCCCATGTTGTTGAATTT	600	
QY	601	ATATGTGACAAATATTTTGGTACTTTATATAGGGATATGGCGCTTTTGGCACTA	660	
DB	601	ATATGTGACAAATATTTTGGTACTTTATATAGGGATATGGCGCTTTTGGCACTA	660	
QY	661	TGGATATTAATCGTATTATATAACAATATCATCTTTGACTAATATATAACAATAAT	720	
DB	661	TGGATATTAATCGTATTATATAACAATATCATCTTTGACTAATATATAACAATAAT	720	
QY	721	TACAATATGTTTGTAAACGTTGAGGTGGCAAAATGTATAAGAGCGCCCTAATAATTA	780	
DB	721	TACAATATGTTTGTAAACGTTGAGGTGGCAAAATGTATAAGAGCGCCCTAATAATTA	780	
QY	781	TTATTTATGAATATAGACTATAGTACAAGTGAACCTTTATTTGGTGATAACTTGGACAT	840	
DB	781	TTATTTATGAATATAGACTATAGTACAAGTGAACCTTTATTTGGTGATAACTTGGACAT	840	
QY	841	ATAAATCTGTATCGTACGAGAACTTTTCTTAAACTAAATATTTAAAGACGCTATTTT	900	
DB	841	ATAAATCTGTATCGTACGAGAACTTTTCTTAAACTAAATATTTAAAGACGCTATTTT	900	
QY	901	AATATTTTTCGTGGCCAAAGTTTCTTGCATATCTATGCCCATTTTACTTTTATCG	960	
DB	901	AATATTTTTCGTGGCCAAAGTTTCTTGCATATCTATGCCCATTTTACTTTTATCG	960	

QY	961	TTCTAGCCTTCTAGTAGCGCTTTGAAACATATAAAAAATCAAAAAATTTGAAAGTAAAAAT	1020	
DB	961	TTCTAGCCTTCTAGTAGCGCTTTGAAACATATAAAAAATCAAAAAATTTGAAAGTAAAAAT	1020	
QY	1021	AGTTTCTTTCATATTTACTCGTATGGATCAATTTCTAGATCAATGTGAATATACAAATC	1080	
DB	1021	AGTTTCTTTCATATTTACTCGTATGGATCAATTTCTAGATCAATGTGAATATACAAATC	1080	
QY	1081	ATTCTGATTTTAAATCATAACTATTCTGATGAGGAACGCTCTATGGTGAATTCGTGAC	1140	
DB	1081	ATTCTGATTTTAAATCATAACTATTCTGATGAGGAACGCTCTATGGTGAATTCGTGAC	1140	
QY	1141	AGTGTCTTGTATTTCTAAGTCTGGATTCGAGTCACAACCTTTTAGTGCAAAATCTATT	1200	
DB	1141	AGTGTCTTGTATTTCTAAGTCTGGATTCGAGTCACAACCTTTTAGTGCAAAATCTATT	1200	
QY	1201	AAAAGAACCCCTATTGATGCAAAAAGTCAATAAATATTTAATATCATNCITTTATTT	1260	
DB	1201	AAAAGAACCCCTATTGATGCAAAAAGTCAATAAATATTTAATATCATNCITTTATTT	1260	
QY	1261	TTACGATCGAGCATGGATACATTTAATAATAAATAAATTTGAAGGAATTTGATCGACA	1320	
DB	1261	TTACGATCGAGCATGGATACATTTAATAATAAATAAATTTGAAGGAATTTGATCGACA	1320	
QY	1321	AGTCATCAAGCTTATCGTCGATCCACATTCCTTAAACGTTAGTATGGCTGCTTTAGAGA	1380	
DB	1321	AGTCATCAAGCTTATCGTCGATCCACATTTAAATAAATCGTTAGTATGGCTGCTTTAGAGA	1380	
QY	1381	AACAAGTGGATCATATAAATTTAGTTTCCCTATCTCTTAAATAATCTATATATACC	1440	
DB	1381	AACAAGTGGATCATATAAATTTAGTTTCCCTATCTCTTAAATAATCTATATATACC	1440	
QY	1441	TCCTAAATCTAATGATCTAACAACACAAATATAAATCTTAGATCTTTTAAAGAAATTTGCA	1500	
DB	1441	TCCTAAATCTAATGATCTAACAACACAAATATAAATCTTAGATCTTTTAAAGAAATTTGCA	1500	
QY	1501	GAATTAATGAGGAGGCAATAAGTCTATGCTGAAGTGGTGGCTTTTC	1546	
DB	1501	GAATTAATGAGGAGGCAATAAGTCTATGCTGAAGTGGTGGCTTTTC	1546	

RESULT 2
 ABK90560
 ID ABK90560 standard; DNA; 1595 BP.
 XX
 AC ABK90560;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Potato proteinase inhibitor 1 (pin1) gene promoter isoform I.
 XX
 KW Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
 KW Controlled Environmental Agriculture; crop cultivation.
 XX
 OS Solanum tuberosum.
 XX
 PN WO200259333-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 18-JAN-2002; 2002WO-US001287.
 XX
 PR 23-JAN-2001; 2001US-0263224P.
 XX
 PA (DAIZ/) DAI Z.
 PA (SHIL/) SHI L.
 PA (HOOK/) HOOKER B S.
 XX
 PI Dai Z, Shi L, Hooker BS;
 XX
 DR WPI; 2002-608457/65.
 XX

New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter isoforms derived from potato, useful in manipulating expression of genes and in Controlled Environmental Agriculture for heterologous protein production.

Claim 2; Fig 1; 43pp; English.

The invention relates to polynucleotides having proteinase inhibitor 1 (pini) or aminotransferase (amt) gene promoter activity. Isoforms of pini and amt gene promoters are useful in manipulating expression of genes, particularly in transformed plant cells. The gene promoters are useful in constructing gene expression vectors and in controlled environmental agriculture for heterologous protein production. The vectors are useful in facilitating the expression and/or secretion of heterologous proteins in cell culture or by crop cultivation. The new gene promoter isoforms provide high level, stable and controllable expression that is temporally, environmentally, or developmentally regulatable. This sequence represents a potato pini gene promoter isoform

Sequence 1595 BP; 510 A; 291 C; 297 G; 497 T; 0 U; 0 Other;

Query Match 88.1%; Score 1362.4; DB 6; Length 1595;
Best Local Similarity 94.1%; Pred. No. 1.2e-297;
Matches 1460; Conservative 0; Mismatches 82; Indels 9;

1	ATCTTTGTTTGA	AAAATTTG	AAAAAGAA	AGCTAG	GACCA	CATG	GCACCTTGG	GGTGC	ACA	CAAT	60	
49	ATCTTTGTTTGA	AAAAATTTG	AAAAAGAA	AGCTAG	GACCA	CATG	GCACCTTGG	GGTGC	ACA	CAAT	108	
61	ATTGTTGCTCT	CCAAATG	TGTTACA	AGGATG	TTTAC	ATCTCG	GGGTACT	TTTAA	AGCTG	AC	120	
109	ATTGTTGCTCT	CCAAATG	TGTTACA	AGGATG	TTTAC	ATCTCG	GGGTACT	TTTAA	AGCTG	AC	168	
121	TAGGCA	CATTAC	CAATTTA	TATTTG	CGGTG	CAATG	AAATTG	CGTG	GCATTTCC	CTCCACTTG	180	
169	CAGGGA	CATTAC	CAATTTA	TATTTG	CGGTG	CAATG	AAATTG	CGTG	GCATTTCC	CTCCACTTG	228	
181	GATTAGT	CGGGCG	AAAGTCA	TGCG	GTATTTAA	TAATCC	ATCAACTAA	GAAGAA	ATGTC	CCACA	240	
229	GATTAGT	CGGGCG	AAAGTCA	TGCG	GTATTTAA	TAATCC	ATCAACTAA	GAAGAA	ATGTC	CCACA	288	
241	AATCTA	AGTTGTTG	AACTGGT	CCGAG	CGTACTCG	GCTAGG	GTGTTG	GGCG	TTTAC	CCCC	300	
289	AATCTA	AGTTGTTG	AACTGGT	CCGAG	CGTACTCG	GCTAGG	GTGTTG	GGCG	TTTAC	CCCC	348	
301	ACCCGGT	GCAC	TG	CAGG	CAC	CA	CAATC	AC	CAGT	CTGC	AG	360
349	ACCCGGT	GCAC	TG	CAGG	CAC	CA	CAATC	AC	CAGT	CTGC	AG	408
361	CATCGA	AGTTAC	ATCCAGT	TAC	GCAC	CCCATATAC	TGTC	GCATCG	TAGTGC	CCCCCTAG	GGCGCAT	420
409	CATCGA	AGTTAC	ATCCAGT	TAC	GCAC	CCCATATAC	TGTC	GCATCG	TAGTGC	CCCCCTAG	GGCGCAT	468
421	CAATG	ACCA	CGTTTGG	CCCTG	AT	CGAG	AGCTGG	GCAC	CGCCCTAT	CGGGGTG	CATGCTG	480
469	CAATG	ACCA	CGTTTGG	CCCG	CGATCG	AAACGTGG	-	CAC	CCGCTTTG	CGGGGTG	CATGCTG	527
481	CCGAC	AGCGTGTAT	GGA	CAGT	TTTGG	GTACTCG	ATAGTGG	CAGAT	AAGTG	AAAGTCA	540	
528	CCCAAC	CGATGTAT	GGA	CAGT	TTTGG	GTACTCG	ATAGTGG	CAGAT	AAAGTCA	587		
541	CAAAAG	CAAGAGG	GAGAAAA	CA	AAAG	AGATCTCA	AGTAG	GCCCATG	TTTGTG	GAATTT	600	
588	CAAAAG	CAAGAGG	GAGAAAA	CA	AAAG	AGATCTCA	AGTAG	GCCCATG	TTTGTG	GAATTT	647	
601	ATATG	TG	GACAAATTA	TTTTTGG	TACTTTAT	ATATAGG	GATATGG	GGCTTTTG	GCACTA	660		
648	ATATG	TG	GACAAATTA	TTTTTGG	TACTTTAT	ATATAGG	GATATGG	GGCTTTTG	GCACTA	707		
661	TGGATTA	TAATCG	TATATATA	TAACA	AAATAT	CATACTTTG	ACTAATTA	TAATAA	CAAAAT	TAAT</		

Qy	721	TACAAATATGATTTGGTAAA	CGTTGAGGTGGCAAAATG	TATAAGAGCGCGCTAATAATAA	780
Db	768	TACAAATATGATTTGGTAAA	CGTTGAGGTGAAAAATG	TATAAGAGCGCGCTAATAATAA	827
Qy	781	TTATTTTATCAATATAGACT	TATAGTACAAGTGAAC	TTTATTTTGGTGATAACTTGGACAT	840
Db	828	TTATTTTATGAAATATAGCC	TATAGTTACAAGTTAA	CTTTATTTTGGTGATTAAC	887
Qy	841	ATAAATCTCTGATCGTGAC	GGAATTTTCTTTAAAACT	ATAATATATTAATAAGCAGCTATTTT	900
Db	888	ATAAATCTCTGATCGTGAC	GGAATTTTCTTTAAAACT	ATAATATATTAATAAGCAGCTATTTT	947
Qy	901	AATATTTTTCGTGGCCAAAG	TTTCTTGCACTATCTAT	TGCCCATTTTAC	960
Db	948	CAGATTTTTCGTGGCCAAAG	TTTCTTGCACTATCTAT	TGCCCATTTTAC	1007
Qy	961	TTCTAGCGTTCTAGGTACG	GGTTTGAACATAAAAAAT	CATAAAAAATGAAAGTAAAAAAT	1020
Db	1008	TTCTAGCGTTCTAGGTACAG	TTTGAACATAAAAAAT	CATAAAAAATGAAAGTAAAAAAT	1067
Qy	1021	AG--	-TTTTTTTTCATATTA	CTCGTATGGAATCAATTTGTTT	1077
Db	1068	AGTTTTTTTTTTTTCATAT	TACTCGTAGGGATCATTTG	TTAGTCAATCTGAAAAATATACAA	1127
Qy	1078	ATCATTTCTGATTTTAAAA	ATCAATCAATTTCTGATG	ATGGAACGCTATGTTGATTCGT	1137
Db	1128	ACATTTCTGATTTTAAAA	ATCACACCAATCTGCAAG	GGGAAGTCTAT---GTGATCCGT	1184
Qy	1138	GACAAGTGTTTGATTTAT	TTCTTAAGTCTGGATTCG	AGTCAACACTTTTGTAGTCAAAATATCT	1197
Db	1185	GACAAGTGTTTGATTTAT	TTCTTAGTCTAGATTGG	AGTCAACACTTTTGTAGTCAAAATATCT	1244
Qy	1198	ATTTAAAGAACCCCTAT	TTGATGCAAAAGTCAATAA	--TATTTAATATCATNCTTTATTT	1255
Db	1245	ATTTAAAGAACCCCTAT	TTGATGCAAAATATCTAT	TTAAAGAACCCCTATTCATGCTTTATTT	1304
Qy	1256	TATTTTTPACGATCGGAG	CATGGATACATTTTACT	TAATTTAAAAATTAATTTGGAAGGAATTGAT	1315
Db	1305	TATTTTTPACGATCGGAG	CATGGATATATTTTACT	TAATTTAAAAATTAATTTGGAAGGAATTTGAT	1364
Qy	1316	CGACAAGTCAATCAAGCT	TATTCGTGATCCACATTT	CCCGCTAACGTTAGTATGGCTGCTTTT	1375
Db	1365	CGACAAGTCAATCAAGCT	TATTCGTGATCCACATTT	AAAAATAACGTTAGTATGGCTGCTTTT	1424
Qy	1376	AGAGAAACAAGTGGATCAT	GTATTAATTTAGTTTTC	CCCTATCTCCTATAAATATCTATAT	1435
Db	1425	AGAGAAACAAGTGGATCAT	GTATTAATTTAGTTTTC	CCCTATAAATATCTCTATAT	1484
Qy	1436	ATACCTCTAAAACTAAAT	GTGATCTAAACACAAAAAT	ATAAACTTTAGATTCTTTAAAGAAA	1495
Db	1485	ATACCTCTAAAACTAAAT	GTGATCTAAACACAAAAAT	ATAAACTTTAGATTCTTTAAAGAAA	1544
Qy	1496	TTGCAGATTTAAATGGAG	GCAATAAGTCTATGGT	GAAAGTTGGTTGCTTTTC	1546
Db	1545	TTGCAGATTTAAATGGAG	GCAATAAGTCTATGGT	GAAAGTTGGTTGCTTTTC	1595

RESULT 3

ABK90561

ID ABK90561 standard; DNA; 1598 BP.

AC ABK90561;

DT 15-NOV-2002 (first entry)

XX
DE Potato proteinase inhibitor 1 (pin1) gene promoter isoform II.

XX Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
KW Controlled Environmental Agriculture; crop cultivation.

OS Solanum tuberosum.

XX PN WO200259333-A2.

[illegible]

XX PD 01-AUG-2002.
 XX PF 18-JAN-2002; 2002WO-US001287.
 XX PR 23-JAN-2001; 2001US-0263224P.
 XX PA (DAIZ/) DAI Z.
 XX PA (SHIL/) SHI L.
 XX PA (HOOK/) HOOKER B S.
 XX PI Dai Z, Shi L, Hooker BS;
 XX DR WPI; 2002-608457/65.
 XX PT New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter
 PT isoforms derived from potato, useful in manipulating expression of genes
 PT and in Controlled Environmental Agriculture for heterologous protein
 PT production.
 XX PS Claim 2; Fig 2; 43pp; English.
 CC The invention relates to polynucleotides having proteinase inhibitor 1
 CC (pin1) or aminotransferase (amt) gene promoter activity. Isoforms of pin1
 CC and amt gene promoters are useful in manipulating expression of genes,
 CC particularly in transformed plant cells. The gene promoters are useful in
 CC constructing gene expression vectors and in Controlled Environmental
 CC Agriculture for heterologous protein production. The vectors are useful
 CC in facilitating the expression and/or secretion of heterologous proteins
 CC in cell culture or by crop cultivation. The new gene promoter isoforms
 CC provide high level, stable and controllable expression that is
 CC temporally, environmentally, or developmentally regulatable. This
 CC sequence represents a potato pin1 gene promoter isoform
 XX SQ Sequence 1598 BP; 507 A; 299 C; 300 G; 492 T; 0 U; 0 Other;
 Query Match 86.3%; Score 1334.4; DB 6; Length 1598;
 Best Local Similarity 93.8%; Pred. No. 2.6e-291;
 Matches 1456; Conservative 0; Mismatches 87; Indels 10; Gaps 6;
 QY 1 ATCTTTGTTTGAAGAAATGGAAAGACGTTAGGACCAATGACACCTGGGTGCAACAAT 60
 DB 49 ATCTTTGTTTGAAGAAATGGAAAGACGTTAGGACCAATGACACCTGGGTGCAACAAT 108
 QY 61 ATTGTTGTCCTCCAAATGTTGTAACAAGATTTACATCTCCGGGTACTTTAAAGCTGAC 120
 DB 109 ATTGTTGTCCTCCAAATGTTGTAACAAGATTTACATCTCCGGGTACTTTAAAGCTGAC 168
 QY 121 TAGGACATTCACCAATTTATTTGCGGTGCAATGAAATGCGTGCATTTCCCTCCACTTGG 180
 DB 169 TAGGACATTCACCAATTTATTTGCGGTGCAATGAAATGTTGTCGATTTCCCTCCACTTGG 228
 QY 181 GATTAGTCGGGGCAAGATCATCGGTATTTAAATCCATCACTAAAGAAATGTCGCCAGA 240
 DB 229 GATTAGTCGGGGCAAGATCATCGGTATTTAAATCCATCACTAAAGAAATGTCGCCAGA 288
 QY 241 AATCTAAGTTGTTGAATGTTGCGGAGCGGTACTCGGCTAGGGTGTGGGGTTTACCC 300
 DB 289 AATCTAAGTTGTTGAATGTTGCGGAGCGGTACTCGGCTAGGGTGTGGGGTTTACCC 348
 QY 301 ACCGGGTGCACTGAGGACCAACCAATCAGGTCATGCAACCTCTACACGACAC 360
 DB 349 ACCGGGTGCACTGAGGACCAACCAATCAGGTCATGCAACCTCTACACGACAC 408
 QY 361 CATCGAAGTTACATCCAGTACGCCCATATATCGTGCATCGTAGTCCCTCAGGGCGCAT 420
 DB 409 CACCGAAGTTACATCCAGTACGCCCATATATCGTGCATCGTAGTCCCTCAGGGCGCAT 468
 QY 421 CAATGACCAAGTTTGGCCCTGATCGAGAGCGTGGCCACCGCTATCGGGTGCATGCTG 480
 DB 469 CAATGACCAAGTTTGGCCCTGATCGAGAGCGTGGCCACCGCTATC-GGGTGCATGCTG 527
 QY 481 CCCAGACGGTGTATGGACAGTTGTTG--CGTACCTCGATAGTGGCAGCATAAGTGAAGT 538

DB 528 CCCAAACGATGTATGGACAGTTGTTGGCGGTACCTTCGATAGTGACGATTAAGTGAAGT 587
 QY 539 CACAAAGCAAGAGGAGGAGAAACAAAGAGAGATCTCAAGTAGGCCCATTTGTTGAAAT 598
 DB 588 CACAAAGCCAGAGGAGGAGAAACCAAGAGAGATCTCAAGTAGGCCCATTTGTTGAAAT 647
 QY 599 TTATATGTGGACAAATTTATTTTGGTACTTTATATATAGGATATGCGGCTTTGGCAC 658
 DB 648 TTATATGTGGACAAATTTATTTTGGTACTTTATATATAGGATATGCGGCTTTGGCAC 707
 QY 659 TATGATATTAATCGTATTTATATAACAATATCATCTTTGACTAATTAATAACAATAAT 718
 DB 708 TACGGATATTAATCGTATTTATATAACAATATCATCTTTGACTAATTAATAACAATAAT 767
 QY 719 ATTACAATATGATTTGTTAAACGTTGAGGTGGGCAAAATGTATAAGAGCGGCTTAATATT 778
 DB 768 ATTACAATATGATTTGTTAAACGTTGAGGTGGGCAAAATGTATAAGAGCGGCTTAATATT 827
 QY 779 AATTATTTTATGATATATAGACTATAGTTTACAAGTCACTTTTATTTGGTGAATCTTGAC 838
 DB 828 AATTATTTTATGATATATAGACTATAGTTTACAAGTCACTTTTATTTGGTGAATCTTGAC 887
 QY 839 ATATAAACTCTGTATCGTGACGGAACTTTCTTAAAACTAAATATTAAGAGCAGCTATT 898
 DB 888 ATATAAACTCTGTAACTGACGGAAATTTCTTAAAACTAAATATTAAGAGCAGCTATT 947
 QY 899 TTAATATTTTGGTGGCCAAAGTTTCTTGCACTATCTATGCGCATTTTACCTTTTAT 958
 DB 948 TTAGATTTTGGTGGCCAAAGTCTCTTGCATCTTATCTATGCGCATTTTACCTTTAT 1007
 QY 959 CGTCTAGCCCTTCTAGGTACGCGTTTGAACATAAAAAATCAATAAAAAATGAAGTAAAAA 1018
 DB 1008 CGTCTAGCCCTTCTAGGTACAGTTTGAACATAAAAAATCAATAAAAAATGAAGTAAAAA 1067
 QY 1019 TTAG--TTTCTTATATCTACTCGTATGATGATCATTTGTTAGATCAATGTGAATATATAC 1075
 DB 1068 TTAGTTTCTTATATCTACTCGTATGATGATCATTTGTTAGATCAATGTGAATATATAC 1127
 QY 1076 AAATCATTTCTGATTTTAAATCATAACTATTTCTGATGATGGGAACTGATGGTATTC 1135
 DB 1128 AAACATTTCTGATTTTAAATCATAACTATTTCTGATGATGGGAACTGAT--GTGATTC 1186
 QY 1136 GTGCAAGTGTGATTTATTTCTAAGTCTGATTTGGAGTGCACACTTTTAGTCAAAATAT 1195
 DB 1187 GTGCAAGTGTGATTTATTTCTAAGTCTGATTTGGAGTGCACACTTTTAGTCAAAATAT 1245
 QY 1196 CTATTAAGAAACCCCTATTTGATGCAAAAGTCAATAAA--TATTTAATATCATCTTTA 1253
 DB 1246 CTATTAAGAAACCCCTATTTGATGCAAAATATCTATTAAGAAACCCCTATTTAATCTTTA 1305
 QY 1254 TTTATTTTACGATCGGAGCATGATACATTTACTTAATTAATAAATGAAGAAATG 1313
 DB 1306 TTTATTTTACGATCGGAGCATGATATTTACTTAATTAATAAATGAAGAAATG 1365
 QY 1314 ATCGAAGTCAATCAAGCTTATCGTGCATCCAGTCCCTTAAGCTAGTATGCTGCTT 1373
 DB 1366 ATCGAAGCTCAATCAAGCTTATCGTGCATCCAGTCCCTTAAGCTAGTATGCTGCTT 1425
 QY 1374 TTAGAGAAACCAAGTGGATCATGTATTAATTTAGTTTTCCTCTATCTCTATAAATATCTAT 1433
 DB 1426 TTAGAGAAACCAAGTGGATCATGTCAATTTAGTTTAAAAAATATCTCTATAAATATCTGT 1485
 QY 1434 ATATACCTCTAAAATCAATGATCATCAACACAAATATTAACCTTAGATCTTTAAGA 1493
 DB 1486 CTATCCCTCTTAAACCAATATACATCAACACAAATATTAACCTTAGATCTTTAAGA 1545
 QY 1494 AATTGCAAAATTAATGAGGCAAAATAGTCTATGTTGAAGTGTGGTCTTTC 1546
 DB 1546 AATTGCAAAATTAATGAGGCAAAATAGTCTATGTTGAAGTGTGGTCTTTC 1598


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XX PF 31-MAY-1991; 91EP-00201344.
XX PR 07-JUN-1990; 90NL-00001293.
XX PA (MOGE-) MOGEN INT NV.
XX PI Woloshuk CP, Melchers LS, Cornelisse BJ, Meulenhoff EJ;
XX PI Selabuuria MB, Vandeneize PJ;
XX DR WPI; 1991-363235/50.
XX DR P-PSDB; AAR15660.
XX PT New antipathogenic proteins obtd. from plants - obtd. by inducing
XX PT resistance in plant to pathogen and prepn. of extract from plant.
XX PS Claim 18; Page 17; 25pp; English.
XX CC The full-length cDNA clone encoding antifungal protein AP20 was obtained
XX CC from a lambda ZAP cDNA library prepared from tobacco mosaic virus-
XX CC infected Samsun NH tobacco leaves. The library was screened with a probe
XX CC for sequences homologous to the NP24 gene of tomato. One positive clone
XX CC was found to contain the complete coding sequence for osmotin except for
XX CC the A-T dinucleotide of the translation initiation codon. With the use of
XX CC PCR, a BamHI site and an A-T dinucleotide was introduced in front of the
XX CC osmotin cDNA; behind the gene a BamHI site was introduced. See also
XX CC AAQ15270. (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 883 BP; 220 A; 198 C; 205 G; 260 T; 0 U; 0 Other;
Query Match 29.1%; Score 450.4; DB 2; Length 883;
Best Local Similarity 85.4%; Pred. No. 8e-92;
Matches 502; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1 ATCTTTGTTTGAATAATTTGAAAGACGTAGGACCACTGACCTTGGTGCAACAAT 60
DB |||||
QY 602 ATCTTTGTTTGAATAATTTGAGAAAATTTGAGAAAATTTGAGAACCAAGTCTTGTGTGCAACAAT 543
DB |||||
QY 61 ATTGTGTCTCCCAATGTTGTAAGGATTGTTACATCTCCGGGTACTTTAAAGTGAC 120
DB |||||
QY 542 ATTGTGTCTCCGATGTAGTACAGGGTTATTACCTCCGGGAACCTTAAGTTCCG 483
DB |||||
QY 121 TAGGACATTCACATTTATATTGTCGGTCATTAAGTTCGTTGGCATTTCCCTCCATTG 180
DB |||||
QY 482 GGGGACATTCGCGGTTTATATTAGCCGTACAAATGAATTCATGGCATTTCCCTCCATTG 423
DB |||||
QY 181 GATTAGTTCGGGCGGAAAGTCAATCGGTATATTAAATCCATCACTAAAGAAATGTCCTCAGA 240
DB |||||
QY 422 GGTAGTTCGGGCGGAAAGTCAATCGGTATATTAAATCCATCACTAAAGAAATGTCCTCAGA 363
DB |||||
QY 241 AATCTAAGTTTGAACCTGTCGAGGCGTACTCGGTAGGTTGTTGGCGTTTACCCC 300
DB |||||
QY 362 AATCTAACCACCTGAATTTGGTCCAAAGCGTATTCAGCCAGGTGTTTGGTGTACCCC 303
DB |||||
QY 301 ACCCGGTGCATTCGAGGACACACATCAATCAGTATGACGAAACCTTACCGACAC 360
DB |||||
QY 302 ACCCGGTGCATTCGAGTCTCCACACAGTCCACGCTTTCGACGTACCCCTACCGACG 243
DB |||||
QY 361 CATCGAAGTTACATCCAGTACGCCATATACGTGCATCGTAGTGCCTAGGCGCAT 420
DB |||||
QY 242 CATTTGAAGTTACATTTAGTACGGCCCCATACAGTGCATTTTAGTACCTCTGTGGCGCAT 183
DB |||||
QY 421 CAATGACCCAGTTTGGCTCGATCGAGAGCTCGGCCACCGCCTATCGGGGTGATGCTG 480
DB |||||
QY 182 TGATCACCCAGTTTGGCTCGATCGAGAGCGCCGCCACCGCCTATCGGGGTGATGCTG 123
DB |||||
QY 481 CCCAGAGCGTGTATGGACAGTTTGGTACCTCGATGAGTGGGACGATAGTGAAGTCA 540
DB |||||
QY 122 CCCAAGCGTGTACGAGACAGTTTTCGGACCTCGATGAGTGGGACGATAGTGAAGTCA 63
DB |||||
QY 541 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCCATGT 588
DB |||||
QY 62 CCAAGGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTTGCCCATGT 15
DB |||||

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RESULT 7
AAQ15270/C
ID AAQ15270 standard; DNA; 884 BP.
XX AC AAQ15270;
XX AC AAQ15270;
XX DT 25-MAR-2003 (revised)
XX DT 16-MAR-1992 (first entry)
XX DE Encodes C-terminally truncated osmotin-like antifungal protein.
XX KW tobacco; osmotic tolerance; AP20; ss.
XX OS Nicotiana tabacum.
XX FH Key Location/Qualifiers
XX FT CDS 17..694
XX FT /*tag= a
XX FT /note= "secretable osmotin-like protein"
XX FN EP460753-A.
XX PD 11-DEC-1991.
XX PF 31-MAY-1991; 91EP-00201344.
XX PR 07-JUN-1990; 90NL-00001293.
XX XX (MOGE-) MOGEN INT NV.
XX PI Woloshuk CP, Melchers LS, Cornelisse BJ, Meulenhoff EJ;
XX PI Selabuuria MB, Vandeneize PJ;
XX DR WPI; 1991-363235/50.
XX DR P-PSDB; AAR15661.
XX PT New antipathogenic proteins obtd. from plants - obtd. by inducing
XX PT resistance in plant to pathogen and prepn. of extract from plant.
XX PS Claim 18; Page 19; 25pp; English.
XX CC The full-length cDNA clone encoding antifungal protein AP20 was obtained
XX CC from a lambda ZAP cDNA library prepared from tobacco mosaic virus-
XX CC infected Samsun NH tobacco leaves (see AAQ15269). To allow secretion of
XX CC the protein into the extracellular space, a T residue was inserted
XX CC between nucleotides 694 and 695 of AAQ15269. This introduces a STOP
XX CC codon. The mutated cDNA thus encodes an osmotin lacking the 20 C-terminal
XX CC amino acids of the wild-type osmotin and which is targeted
XX CC extracellularly. (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 884 BP; 220 A; 198 C; 205 G; 261 T; 0 U; 0 Other;
Query Match 29.1%; Score 450.4; DB 2; Length 884;
Best Local Similarity 85.4%; Pred. No. 8e-92;
Matches 502; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1 ATCTTTGTTTGAATAATTTGAAAGACGTAGGACCACTGACCTTGGTGCAACAAT 60
DB |||||
QY 602 ATCTTTGTTTGAATAATTTGAGAAAATTTGAGAAAATTTGAGAACCAAGTCTTGTGTGCAACAAT 543
DB |||||
QY 61 ATTGTGTCTCCCAATGTTGTAAGGATTGTTACATCTCCGGGTACTTTAAAGTGAC 120
DB |||||
QY 542 ATTGTGTCTCCGATGTAGTACAGGGTTATTACCTCCGGGAACCTTAAGTTCCG 483
DB |||||
QY 121 TAGGACATTCACATTTATATTGTCGGTCATTAAGTTCGTTGGCATTTCCCTCCATTG 180
DB |||||
QY 482 GGGGACATTCGCGGTTTATATTAGCCGTACAAATGAATTCATGGCATTTCCCTCCATTG 423
DB |||||
QY 181 GATTAGTTCGGGCGGAAAGTCAATCGGTATATTAAATCCATCACTAAAGAAATGTCCTCAGA 240
DB |||||
QY 422 GGTAGTTCGGGCGGAAAGTCAATCGGTATATTAAATCCATCACTAAAGAAATGTCCTCAGA 363
DB |||||
QY 241 AATCTAAGTTTGAACCTGTCGAGGCGTACTCGGTAGGTTGTTGGCGTTTACCCC 300
DB |||||
QY 362 AATCTAACCACCTGAATTTGGTCCAAAGCGTATTCAGCCAGGTGTTTGGTGTACCCC 303
DB |||||
QY 301 ACCCGGTGCATTCGAGGACACACATCAATCAGTATGACGAAACCTTACCGACAC 360
DB |||||
QY 302 ACCCGGTGCATTCGAGTCTCCACACAGTCCACGCTTTCGACGTACCCCTACCGACG 243
DB |||||
QY 361 CATCGAAGTTACATCCAGTACGCCATATACGTGCATCGTAGTGCCTAGGCGCAT 420
DB |||||
QY 242 CATTTGAAGTTACATTTAGTACGGCCCCATACAGTGCATTTTAGTACCTCTGTGGCGCAT 183
DB |||||
QY 421 CAATGACCCAGTTTGGCTCGATCGAGAGCTCGGCCACCGCCTATCGGGGTGATGCTG 480
DB |||||
QY 182 TGATCACCCAGTTTGGCTCGATCGAGAGCGCCGCCACCGCCTATCGGGGTGATGCTG 123
DB |||||
QY 481 CCCAGAGCGTGTATGGACAGTTTGGTACCTCGATGAGTGGGACGATAGTGAAGTCA 540
DB |||||
QY 122 CCCAAGCGTGTACGAGACAGTTTTCGGACCTCGATGAGTGGGACGATAGTGAAGTCA 63
DB |||||
QY 541 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCCATGT 588
DB |||||
QY 62 CCAAGGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTTGCCCATGT 15
DB |||||

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QY 241 AATCTAAGTTGTTGAACCTGTCGAGCGCTACTCGGCTAGGCTGTTGGCGGTTTACCCC 300
 DB 362 AATCTAACCACCTGAATTGGTCCAAAGCGTATTACAGCCAAAGTGTGTTGGTGGTTTACCCC 303
 QY 301 ACCCGGTGCTAGCAGACACACCAACATCACCAGTCTACGACGACCTCTACGACGAC 360
 DB 302 ACCCGGTGCTAGCAGTCTAGGACTCCACCACAGTCAACCGGTTTGGCCAGTACCCCTACGACGAC 343
 QY 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCTAGTGCCTAGGCGCAT 420
 DB 242 CATTTGAAGTTACAATTAGTACGGCCCATACAGTGCCTATTTAGTACCTCGTGGCGCAT 183
 QY 421 CAATGACCCAGTTTGGCTCGATCGAGAGCTCGGCGCACCGCTATCGGGGTGCTGCTG 480
 DB 182 TGATCAACCCAGTTTGGCTCGATCGAGAGCTCGGCGCACCGCTATCGGGGTGCTGACGCGC 123
 QY 481 CCCAGAGCGTGTATGGACAGTTGTTGGTACCTCGATAGTGGCAGCATAGTCAAAAGTCA 540
 DB 122 CCCAAACCGGTGTACGGACAGTTGTTCCGACCTCGATAGTGGCAGCATAGTCAAAAGTCA 63
 QY 541 CAAAGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCATGT 588
 DB 62 CCAAGGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTTGCCATGT 15

RESULT 8

AAV68641/c
 ID AAV68641 standard; DNA; 741 BP.

AC AAV68641;

XX 12-MAR-1999 (first entry)

XX Nucleotide sequence of the osmotin AP24.

XX Osmotin AP24; beta-(1,6)-glucanase; bG; chimeric DNA;
 KW anti-fungal composition; transgenic plant; pathogen resistant; ds.

XX Nicotiana tabacum.

XX Key Location/Qualifiers
 FH 1..741
 FT /*tag= a
 FT /product= "osmotin AP24"

XX WO9849331-A1.

XX 05-NOV-1998.

XX 27-APR-1998; 98WO-EP002580.

XX 29-APR-1997; 97EP-00201254.

XX (MOGE-) MOGEN INT NV.

XX Stuiver MH, Lageweg W, Van Deventer- Troost JPE, Custers JHHV;

XX WPI; 1999-024066/02.

XX P-PSDB; AAW80986.

XX Isolated protein with beta-glucanase activity - is isolated from edible
 PT fungus and used to produce pathogen resistant plants.

PS Claim 13; Page 27-28; 47pp; English.

XX This is the nucleotide sequence encoding the Nicotiana tabacum osmotin
 CC AP24, used in the method of the invention in conjunction with beta-(1,6)-
 CC glucanase (bG) to produce a chimeric DNA. Osmotin AP24 and beta-(1,6)-
 CC glucanase (bG) can be used in an anti-fungal composition. The chimeric
 CC DNA sequences can be transferred into plants to make them pathogen
 CC resistant

SQ Sequence 741 BP; 182 A; 173 C; 178 G; 208 T; 0 U; 0 Other;
 Query Match 29.0%; Score 448.4; DB 2; Length 741;
 Best Local Similarity 85.3%; Pred. No. 2.1e-91;
 Matches 500; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
 QY 1 ATCTTTGTTTGAAGAAATGGAAGAAAGCTAGGACACATGACCTTGGTGGCAACAAT 60
 DB 586 ATCTTTGTTTGAAGAAATTTGAGAAATGAGAACCCACAGGTCCTTTGTGTGCAACAAT 527
 QY 61 ATTGTGTCCTCCAAATGTGTACAAGGATTTTACATCTCTCCGGGACTTTTAAGCTGAC 120
 DB 526 ATTGTGTCCTCCGAAATGTAGTACAAGGTTATTACATCTCTCCGGGAACCTTAAGTTGCG 467
 QY 121 TAGGACATTCACCATTTATATTTCCCGTGCAATGCAATGCGTGGCATTTCCCTCCACTTG 180
 DB 466 GGGGACATTCGCCCGTTTATATTAGCCGTACAAATGAATTCATGTCATTTCCCTCCACTAG 407
 QY 181 GATTAGTCGGGGCGAAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGTCCAGA 240
 DB 406 GGTTAGTCGGGGCGAAAGTCAATCGGAATTTGATTCATCAACTAAAGAAATGTCCAGA 347
 QY 241 AATCTAAGTTGTTGAACCTGTCGAGCGCTACTCGGCTAGGCTGTTGGCGGTTTACCCC 300
 DB 346 AATCTAACCACCTGAATTGGTCCAAAGCGTATTACAGCCAAAGTGTGTTGGTGGTTTACCCC 287
 QY 301 ACCCGGTGCTAGCAGGACACACCAATCACCAGTCAATGACGAACTCTACGACGAC 360
 DB 286 ACCCGGTGCTAGGACTCCACCACAGTCAACCGGTTTGGCAGCTACCCCTACGACGAC 227
 QY 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTGCATCGTGCCTAGGCGCAT 420
 DB 226 CATCGAAGTTACAATTAGTACGGCGCCCATACACAGTGCCTATTTAGTACCTCGTGGCGCAT 167
 QY 421 CAATGACCCAGTTTGGCTCGATCGAGAGCTCGGCGCACCGCTATCGGGGTGCTGCTG 480
 DB 166 TGATCAACCCAGTTTGGCTCGATCGAGAGCTCGGCGCACCGCTATCGGGGTGCTGACGCGC 107
 QY 481 CCCAGAGCGTGTATGGACAGTTTGGCTACCTCGATAGTGGCAGCATAGTCAAAAGTCA 540
 DB 106 CCCAAACCGGTGTACGGACAGTTTTCGACCTCGATAGTGGCAGCATAGTCAAAAGTCA 47
 QY 541 CAAAGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCAT 586
 DB 46 CCAAGGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTTGCCAT 1

RESULT 9

AAQ21414/c
 ID AAQ21414 standard; DNA; 1004 BP.

XX AAQ21414;

XX 10-JUN-1992 (first entry)

XX Encodes osmotin-like protein from tobacco plant.

XX drought tolerance; salt tolerance; environmental stress; ss.

XX Nicotiana tabacum.

XX Key Location/Qualifiers
 FH 18..80
 FT /*tag= a
 FT mat_peptide 81..773
 FT /*tag= b
 FT /product= "osmotin_like_protein"

XX JP04018099-A.

XX 22-JAN-1992.

XX 10-MAY-1990; 90JP-00121816.

PR	18-JUN-1999;	99US-0139750P.	PR	27-AUG-1999;	99US-0151065P.
PR	18-JUN-1999;	99US-0139763P.	PR	27-AUG-1999;	99US-0151066P.
PR	21-JUN-1999;	99US-0139817P.	PR	30-AUG-1999;	99US-0151080P.
PR	21-JUN-1999;	99US-0139899P.	PR	31-AUG-1999;	99US-0151130P.
PR	23-JUN-1999;	99US-0140333P.	PR	01-SEP-1999;	99US-0151438P.
PR	23-JUN-1999;	99US-0140354P.	PR	07-SEP-1999;	99US-0151930P.
PR	24-JUN-1999;	99US-0140695P.	PR	10-SEP-1999;	99US-0152363P.
PR	28-JUN-1999;	99US-0140823P.	PR	13-SEP-1999;	99US-0153070P.
PR	29-JUN-1999;	99US-0140991P.	PR	15-SEP-1999;	99US-0153758P.
PR	30-JUN-1999;	99US-0141287P.	PR	16-SEP-1999;	99US-0154018P.
PR	01-JUL-1999;	99US-0141842P.	PR	22-SEP-1999;	99US-0154039P.
PR	01-JUL-1999;	99US-0142154P.	PR	22-SEP-1999;	99US-0154779P.
PR	02-JUL-1999;	99US-0142055P.	PR	23-SEP-1999;	99US-0155139P.
PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-0155486P.
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.
PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0142977P.	PR	29-SEP-1999;	99US-0156596P.
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157753P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144884P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0144884P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	21-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.
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PR	22-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146389P.	PR	26-OCT-1999;	99US-0161920P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161992P.
PR	04-AUG-1999;	99US-0147204P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162142P.
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PR	05-AUG-1999;	99US-0147260P.			
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PR	06-AUG-1999;	99US-0147416P.			
PR	09-AUG-1999;	99US-0147935P.			
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PR	10-AUG-1999;	99US-0148319P.			
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PR	12-AUG-1999;	99US-0148565P.			
PR	13-AUG-1999;	99US-0148684P.			
PR	16-AUG-1999;	99US-0149368P.			
PR	17-AUG-1999;	99US-0149175P.			
PR	18-AUG-1999;	99US-0149426P.			
PR	20-AUG-1999;	99US-0149722P.			
PR	20-AUG-1999;	99US-0149723P.			
PR	23-AUG-1999;	99US-0149929P.			
PR	23-AUG-1999;	99US-0149902P.			
PR	23-AUG-1999;	99US-0149930P.			
PR	25-AUG-1999;	99US-0150566P.			
PR	26-AUG-1999;	99US-0150884P.			

Query Match 13.5%; Score 208.2; DB 3; Length 906;

Best Local Similarity 62.8%; Pred. No. 3.8e-37;

Matches 381; Conservative 0; Mismatches 208; Indels 18; Gaps 3;

QY 1 ATCTTTGTTGAAAAATGGAAACGCTAGGACCCATG-----GACCTTGGGTGC 54

Db 616 ATCTCTGCTTAAAGAACTCTTGAGTAGTCAGTATCGCTACATGATCCCTGACCGTTCGTAC 557

QY 55 AACAAATATGTTGCTCTCCAAATGGTACAGGATTTGTTTACCTCCCGGTACTTTAA 114

Db 556 AACAGTATTTGGTTTCGCTGGAATACAGTACACGGGTTGTTGCATCCACCTGGGCTCTCA 497

QY 115 GCTGACTAGGACATTCACCATTTATTTGCGGTGTCATTTGAATTCGTTGGCAATTCCTC 174

Db 496 ACACGTTTGGACATTTGTCGTTTATGTTCTGCGGTACATAGTATCCGATGGCAGTTC---- 441

QY 175 CACTTGGATTAGTCGGGGGGAAGTCATCGGTATATTAAATCCCACTCAACTAAAGATGT 234

Db 440 -----GAACCTAGTTGGGTAACTCCATAGGTATGTTAAATCCATCGCAAGTGAGATAT 386

QY 235 CCCAGAAATCTAAGTTGTTGAACTGGTCCGAGGCGCTACTCGGCTAGGTGTTTGGCGGTT 294


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Db      385 CGTAGAGTCTAAGTGTGTTGAATGTTCAAGCGTACTCAGCCAACTGTTGGTGGGT 326
QY      295 TACCCACCCCGGTGCACCTGCAGGACACCAACCAATCACCAGTCTATGACGAACTCTAC 354
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QY      355 GAGCACCATCGAAGTTACATCCAGTACGACCCCATATAGTGCCTATCGTAGTGGCCCTAG 414
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QY      415 GCGCATCAATGACCCACACCTTTGGCTCGATCGAGACGTGCGGCCACCGCTATCGGGGTGCG 474
Db      205 CGACATCTAGCTCCATGATGTCGCGCAGCATCTAGAGGTGCGCCACCTCC---AGGGCTTG 149
QY      475 ATGCTGCCAGACGCTGTATGACAGTTGTTGCGTACCTCGATAGTGCACGACATAAGTGA 534
Db      148 CGCGAGCCCAACACCGGTGTAACTACATTGGTTTAGGATTTGGAATGTGGCGGCTGTTGGG 89
QY      535 AAGTCACAAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGTG 594
Db      88 TGGAGATGAGCAAAAGTGCAGAAATATGAAGTAGAGACCAAGGTTTCCCATTTTTT 29
QY      595 AAATTTA 601
Db      28 AGTTCTA 22

RESULT 11
AAC47227/c
ID AAC47227 standard; DNA; 902 BP.
XX AC AAC47227;
XX XX
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 53029.
XX KW Hybridisation assay; Genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway; metabolic pathway;
XX KW promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX XX
XX PN EP:033405-A2.
XX XX
XX PD 06-SEP-2000.
XX XX
XX PF 25-FEB-2000; 2000EP-00301439.
XX XX
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
XX PR 23-MAR-1999; 99US-0125788P.
XX PR 29-MAR-1999; 99US-0126264P.
XX PR 29-MAR-1999; 99US-0126785P.
XX PR 01-APR-1999; 99US-0127462P.
XX PR 06-APR-1999; 99US-0128234P.
XX PR 08-APR-1999; 99US-0128714P.
XX PR 16-APR-1999; 99US-0129845P.
XX PR 19-APR-1999; 99US-0130077P.
XX PR 21-APR-1999; 99US-0130449P.
XX PR 23-APR-1999; 99US-0130510P.
XX PR 23-APR-1999; 99US-0130891P.
XX PR 28-APR-1999; 99US-0131449P.
XX PR 30-APR-1999; 99US-0132048P.
XX PR 30-APR-1999; 99US-0132407P.
XX PR 04-MAY-1999; 99US-0132484P.
XX PR 05-MAY-1999; 99US-0132485P.
XX PR 06-MAY-1999; 99US-0132486P.
XX PR 06-MAY-1999; 99US-0132487P.
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XX PR 27-MAY-1999; 99US-0136392P.
XX PR 28-MAY-1999; 99US-0136782P.
XX PR 01-JUN-1999; 99US-0137222P.
XX PR 03-JUN-1999; 99US-0137528P.
XX PR 04-JUN-1999; 99US-0137502P.
XX PR 07-JUN-1999; 99US-0137724P.
XX PR 08-JUN-1999; 99US-0138094P.
XX PR 10-JUN-1999; 99US-0138540P.
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XX PR 18-JUN-1999; 99US-0139750P.
XX PR 18-JUN-1999; 99US-0139763P.
XX PR 21-JUN-1999; 99US-0139817P.
XX PR 22-JUN-1999; 99US-0139899P.
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XX PR 23-JUN-1999; 99US-0140354P.
XX PR 24-JUN-1999; 99US-0140695P.
XX PR 28-JUN-1999; 99US-0140823P.
XX PR 29-JUN-1999; 99US-0140991P.
XX PR 30-JUN-1999; 99US-0141287P.
XX PR 01-JUL-1999; 99US-0141842P.
XX PR 01-JUL-1999; 99US-0142154P.
XX PR 02-JUL-1999; 99US-0142055P.
XX PR 06-JUL-1999; 99US-0143290P.
XX PR 08-JUL-1999; 99US-0143803P.
XX PR 09-JUL-1999; 99US-0143920P.
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XX PR 13-JUL-1999; 99US-0143542P.
XX PR 14-JUL-1999; 99US-0143624P.
XX PR 15-JUL-1999; 99US-0144005P.
XX PR 16-JUL-1999; 99US-0144085P.
XX PR 16-JUL-1999; 99US-0144086P.
XX PR 19-JUL-1999; 99US-0144325P.
XX PR 19-JUL-1999; 99US-0144331P.
XX PR 19-JUL-1999; 99US-0144332P.
XX PR 19-JUL-1999; 99US-0144333P.
XX PR 19-JUL-1999; 99US-0144334P.
XX PR 19-JUL-1999; 99US-0144335P.
XX PR 20-JUL-1999; 99US-0144352P.
XX PR 20-JUL-1999; 99US-0144632P.
XX PR 20-JUL-1999; 99US-0144884P.
XX PR 21-JUL-1999; 99US-0144814P.
XX PR 21-JUL-1999; 99US-0145086P.
XX PR 21-JUL-1999; 99US-0145088P.
XX PR 22-JUL-1999; 99US-0145085P.
XX PR 22-JUL-1999; 99US-0145087P.
XX PR 22-JUL-1999; 99US-0145089P.
XX PR 22-JUL-1999; 99US-0145192P.
XX PR 23-JUL-1999; 99US-0145145P.
XX PR 23-JUL-1999; 99US-0145218P.
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PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	28-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161992P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
PR	04-AUG-1999;	99US-0147302P.	Query Match 13.4%; Score 207.8; DB 3; Length 902;		
PR	05-AUG-1999;	99US-0147302P.	Best Local Similarity 63.5%; Pred. No. 4.7e-37;		
PR	05-AUG-1999;	99US-0147260P.	Matches 355; Conservative 0; Mismatches 192; Indels 12; Gaps 2;		
PR	06-AUG-1999;	99US-0147303P.	QY	43	GACCTTGGTGCACAAATATTGTTGCTCCTCAAAATGGTACAAAGGATTGTTACATCCTC 102
PR	06-AUG-1999;	99US-0147303P.	DB	564	GACCTTGGTGCACAAAGTATTGGTCTCGTCTGAATACAGTACACGGTGTGTTGATCCAC 505
PR	09-AUG-1999;	99US-0147416P.	QY	103	CGGGTACTTTAAGCTGACTAGGACATTCACCATTTATATTTTCCCGTCGATTGAAATTCGT 162
PR	09-AUG-1999;	99US-0147432P.	DB	504	CTGGGGCTCTCAACACGTTTGGACATTTGTCGTTTATGTCGCGGTACATAGTATCCGAT 445
PR	11-AUG-1999;	99US-0148319P.	QY	163	GGCATTTCCCTCCACTTCGATTAGTCGGGGCGAAAGTCATCGGTATATTAATCCATCA 222
PR	12-AUG-1999;	99US-0148341P.	DB	444	GGCAGTTC-----GAACTAGTGGGCTAAACTCCATAGGTATGTTAAATCCATCGA 394
PR	13-AUG-1999;	99US-0148565P.	QY	223	CTAAAGAAATGTCCAGAAATCTAAGTTGTTGAACTGGTCCGAGGCGTACTCGGCTAGGG 282
PR	13-AUG-1999;	99US-0148684P.	DB	393	CAAGTGAGTATCGTAGAGTCTAAGTTGTTGAAATGGTTTCAAAGCGTACTCAGCCACG 334
PR	16-AUG-1999;	99US-0149368P.	QY	283	TGTTTGGCGGTTTACCCACCGGTTGACCTCGAGGACACCAACCAATCACCAGTCATGC 342
PR	17-AUG-1999;	99US-0149175P.	DB	333	TGTTTGGTGGTGTCTCCAGCCAGTACATTCGAGTCCACCACTCGAGTCACCGATTGGC 274
PR	18-AUG-1999;	99US-0149426P.	QY	343	ACGAACCTCTACCAAGCACCATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCG 402
PR	20-AUG-1999;	99US-0149723P.	DB	273	ATCGGCCACGACCTGAGAGTCAAGTTACATTTGGTCTTACCCCAATCGTGCCATT 214
PR	20-AUG-1999;	99US-0149929P.	QY	403	TAGTCCCTTACGGCGCATCAATGACCCACGTTTGGCTTCGATCGAGAGCTCGGCCACCGC 462
PR	23-AUG-1999;	99US-0149902P.	DB	213	TAGTCCCGCGGACATCTAGCCTCCATGATTCGCCAGCATCTAGAGCTCGGCCACCTC 154
PR	23-AUG-1999;	99US-0149930P.	QY	463	CTATCGGGTGCATGCTGCCAGCGGTGATGGACAGTTGTTGCTACCTCGATAGTGG 522
PR	25-AUG-1999;	99US-0150566P.	DB	153	C---AGGGCTTGGCGCAGCCCAACGCGGTAACTACATTTGGTTTAGGATTTTGGATGG 97
PR	26-AUG-1999;	99US-0150884P.	QY	523	CAGCATAAGTGAAGTCAAAAAGCAAGAGGGAGAAACAAAGAGATCTCAAGTAGC 582
PR	27-AUG-1999;	99US-0151065P.	DB	96	CGGCTGTTGGGTGGAGATGAGCAAAAGTGGGAAATATGAAAGTAGAGACCAAGAGGT 37
PR	27-AUG-1999;	99US-0151066P.	QY	583	CCATGTTTGTGAATTTA 601
PR	30-AUG-1999;	99US-0151080P.	DB	36	TTGCCATTTTGTAGTTCTA 18
PR	31-AUG-1999;	99US-0151303P.	RESULT 12		
PR	01-SEP-1999;	99US-0151438P.	AB214313/c		
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PR	10-SEP-1999;	99US-0152363P.	XX		
PR	13-SEP-1999;	99US-0153070P.	AC AB214313;		
PR	15-SEP-1999;	99US-0153758P.	XX		
PR	16-SEP-1999;	99US-0154018P.	XX		
PR	20-SEP-1999;	99US-0154039P.	DT 21-JAN-2003 (first entry)		
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PR	08-OCT-1999;	99US-0158232P.	XX		
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PR	21-OCT-1999;	99US-0160767P.	XX		
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PR	22-OCT-1999;	99US-0160980P.	XX		
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Db 415 GGCAGTTC-----GAATAGTGGGCTAAACTCCATAGGTATGTTAAATCCATCGA 365
 QY 223 CTAAGAATAATGCCAGAAATCTAAGTTGTTGAATCGTCCGAGGCGTACTCGGCTAGGG 282
 Db 364 CAAGTGAGATATCGTAGAGTCTAAGTTGTTGAATGTTCAAGCGTACTCAGCCACG 305
 QY 283 TGTGTTGGGGTTTACCCACCGGTGCACTGCAGGACACCAACCAATCAACAGTCAATGC 342
 Db 304 TGTGTTGGGGTGTCCCGAGCCAGTACATTTGGAGTCCACCACTGCAGTCCACAGTTGGC 245
 QY 343 ACGAACCTCTACCAAGCATTGCAAGTTTACATCCAGTACGACCCCATATACGTGCGCATCG 402
 Db 244 ATCGGCCACGACCTGAGAGTCAAGTTACATTTGTCCTACCCCAATCCGTGCGCATTT 195
 QY 403 TAGTGCCTTACGCGCATCAATACCAACCGTTGGCTCGATCGAGACGTGCGCCACCGC 462
 Db 184 TAGTGCCTGCGCGCATCTAGCCTCCATGATTGGCCAGCATCTAGACGTGCGGCCACCTC 125
 QY 463 CTATCGGGGTGATGCTGCCAGACGGGTGATGGACAGTTGTTGCGTACCTCGATAGTGG 522
 Db 124 C---AGGCTTGGCGGAGCCACACGGTGTAATCTACATTTGGTTAGGATTTGGAATGTTG 68
 QY 523 CAGCATAAGTGAAGTCAAAAAGCAAGAGGAGGAGAAAACAAAAGAGATCTCAAG 578
 Db 67 CGGCTGTTGGCGTGAGATGAGCAAAAGTGGGAAATATGAAAGTAGAGACCAAG 12

RESULT 14

ADA68525/c

ID ADA68525 standard; DNA; 735 BP.

XX AC ADA68525;

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XX SQ Sequence 735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;
 Query Match 13.4%; Score 207.2; DB 7; Length 735;
 Best Local Similarity 64.6%; Pred. No. 6.1e-37;
 Matches 346; Conservative 0; Mismatches 178; Indels 12; Gaps 2;
 QY 43 GACCTTGGGTGCAACATATTTGTTGCTCCTCAAAATGTTGGTACAGAGATTTGTAATCCTC 102
 Db 535 GACCTTGGGTGCAACATATTTGTTGCTCCTCAAAATGTTGGTACAGAGATTTGTAATCCTC 476
 QY 103 CGGGTACTTTAAGCTGACTAGGACATTCACCATTTATTTGCGGTGCAATGATTCGCT 162
 Db 475 CTGGGGCTCTCAACACGTTTGACATTTGTCGTTTATGTTCTCGGTACATGATTCGAT 416
 QY 163 GGCATTTCCCTCCACTTGGATTAGTTCGGGGGGAAGTCAATCGGTATATTTAAATCCATCAA 222
 Db 415 GGCAGTTC-----GAATAGTGGGCTAAACTCCATAGGTATGTTAAATCCATCGA 365
 QY 223 CTAAGAATAATGCCAGAAATCTAAGTTGTTGAATCGTCCGAGGCGTACTCGGCTAGGG 282
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 QY 343 ACGAACCTCTACGAGCACCATCGAAGTTACATCCAGTACGACCCCATATATAGTCCCATCG 402
 Db 244 ATCGGCCACGACCTGAGAGTCAAGTTTACAAATTTGGTCTACCCCAATCCGTGCGCATTT 185
 QY 403 TAGTGCCTTACGCGCATCAATGACCCACGTTTGGCTCGATCGAGACGTGCGGCCACCGC 462
 Db 184 TAGTGCCTGCGCGCATCTAGCCTCCATGATTTGGCCAGCATCTAGAGTCCGACCTC 125
 QY 463 CTATCGGGTTCGATGCTGCCAGACGGGTGATGGACAGTTGTTGCGTACCTCGATAGTGG 522
 Db 124 C---AGGCTTGGCGGAGCCACACGGTGTAATCTACATTTGGTTAGGATTTGGAATGTTG 68
 QY 523 CAGCATAAGTGAAGTCAAAAAGCAAGAGGAGGAGAAAACAAAAGAGATCTCAAG 578
 Db 67 CGGCTGTTGGCGTGAGATGAGCAAAAGTGGGAAATATGAAAGTAGAGACCAAG 12

RESULT 15

ABN98566/c

ID ABN98566 standard; DNA; 950 BP.

XX AC ABN98566;

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Arabidopsis thaliana expressed polynucleotide SEQ ID NO 334.
 Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
 disease; crop; thale cress; tolerance factor; insect; pathogen;
 nutrition; ds.
 Arabidopsis thaliana.
 US2002023281-A1.
 21-FEB-2002.
 26-JAN-2001; 2001US-00770445.
 27-JAN-2000; 2000US-0178472P.
 (GORL/) GORLACH J.
 (ANY/) AN Y.
 (HAMI/) HAMILTON C M.
 (PRIC/) PRICE J L.
 (RAIN/) RAINES T M.

Claim 6; SEQ ID NO 566; 899pp; English.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

PA (YUY/) YU Y.
 PA (NAME/) RAMEKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX
 PI Goralach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 XX
 DR WPI; 2002-403163/43.
 XX
 PT New Arabidopsis thaliana nucleic acid for identifying homologous genes,
 PT producing compositions that modulate the expression or function of its
 PT encoded protein, and mapping functional regions of protein.
 XX
 PS Claim 1; SEQ ID NO 334; 49pp + Sequence Listing; English.
 XX
 CC The invention relates to an Arabidopsis thaliana nucleic acid (I)
 CC comprising a sequence capable of hybridising under stringent conditions
 CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
 CC given in the specification or its fragment. A polypeptide (II) encoded by
 CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
 CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
 CC useful for screening a candidate agent for its biological effect. (I) is
 CC useful in identifying homologous or related genes, in producing
 CC compositions that modulate the expression or function of its encoded
 CC protein, mapping functional regions of the protein and in studying
 CC associated physiological pathways. (I) is also useful for the genetic
 CC manipulation of cells, particularly plant cells. (I) is also useful in
 CC screening assays of various plant strains to determine the strains that
 CC are best capable of withstanding a particular disease or environmental
 CC stress. (II) and (III) are useful for screening of biologically active
 CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
 CC pathways. The screened agents are useful in improved methods of treating
 CC crops to prevent or treat disease. (II) are also useful in screening
 CC programs to identify agents that mimic or enhance the action of tolerance
 CC factors. Such agents are useful in improved methods of treating crops to
 CC enhance their tolerance to environmental stress. (I) is also useful for
 CC enhancing or inhibiting production of a biosynthetic product in a plant.
 CC (III) is useful for identifying other mediators that may induce
 CC expression of proteins of interest, for establishing the extent to which
 CC any specific insect and/or pathogen is responsible for damage to a
 CC particular plant, for identifying other mediators that enhance or induce
 CC tolerance to environmental stress, for identifying factors involved in
 CC biosynthetic pathways of nutritional, commercial or medicinal value and
 CC for identifying productions of nutritional, commercial or medicinal
 CC value. (IV) is useful in the study of genetic function and regulation,
 CC for alteration of the cellular metabolism and for screening compounds
 CC that may affect the biological function of the gene or gene products.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=99909770445
 XX
 SQ Sequence 950 BP; 261 A; 225 C; 213 G; 251 T; 0 U; 0 Other;

Query Match 13.4%; Score 207.2; DB 6; Length 950;
 Best Local Similarity 64.6%; Pred. No. 6.5e-37;
 Matches 346; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

QY 43 GACCTTGGTGCACAAATATTGTCCTCCAATGTGGTACAGAGATTCTTACATCCTC 102
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 Db 543 GACCGTTCTGTACAAACAGTATTGGTTGCTCTGAATACAGTACACGGGTCTTGCATCCAC 484

Search completed: August 18, 2004, 07:59:11
 Job time : 555.632 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 06:27:01 ; Search time 119.074 Seconds
(without alignments)
7205.239 Million cell updates/sec

Title: US-10-051-307-3
Perfect score: 1546
Sequence: 1 atctttgttgaaaaattg.....tggtagtggtggttttc 1546

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	450.4	29.1	883	1	US-07-828-798C-4
C 3	450.4	29.1	883	2	US-08-315-868A-4
C 4	450.4	29.1	883	3	US-08-495-819B-4
C 5	450.4	29.1	884	1	US-07-828-798C-5
C 6	450.4	29.1	884	2	US-08-315-868A-5
C 7	450.4	29.1	884	3	US-08-495-819B-5
C 8	180.6	11.7	875	4	US-09-589-733C-4
C 9	159.2	10.3	900	1	US-08-181-271A-4
C 10	159.2	10.3	900	1	US-08-449-315-4
C 11	159.2	10.3	900	1	US-08-444-803-4
C 12	159.2	10.3	900	1	US-08-449-043-4
C 13	159.2	10.3	900	1	US-08-456-265A-4
C 14	159.2	10.3	900	1	US-08-455-416-4
C 15	159.2	10.3	900	1	US-08-455-244-4
C 16	159.2	10.3	900	1	US-08-454-876-4
C 17	159.2	10.3	900	2	US-08-457-364-4
C 18	159.2	10.3	900	2	US-08-456-262-4
C 19	159.2	10.3	900	2	US-08-456-240-4
C 20	159.2	10.3	900	2	US-08-455-736-4
C 21	159.2	10.3	900	2	US-08-971-217-4
C 22	159.2	10.3	900	3	US-09-350-600-4
C 23	159.2	10.3	900	4	US-09-350-234-4
C 24	152.6	9.9	910	4	US-09-096-234-4
C 25	124.8	8.1	894	1	US-08-178-708-7
C 26	124.8	8.1	894	1	US-08-457-552-7
C 27	124.8	8.1	894	1	US-08-456-430-7

C 28	124.8	8.1	894	2	US-08-994-418-7
C 29	124.8	8.1	894	5	PCT-US95-00432-7
C 30	101	6.5	1309	6	5221624-4
C 31	94	6.1	621	4	US-09-224-514A-1
C 32	94	6.1	621	6	5221624-31
C 33	92.8	6.0	621	4	US-09-224-514A-9
C 34	83	5.4	624	2	US-08-426-599B-3
C 35	76.4	4.9	624	2	US-08-426-599B-1
C 36	73.8	4.8	2051	1	US-08-482-037A-2
C 37	67.8	4.4	230	3	US-09-589-733C-28
C 38	52	3.4	636	3	US-08-998-416-1137
C 39	51.6	3.3	832	4	US-09-621-976-2813
C 40	51.2	3.3	6152	3	US-08-973-462-1
C 41	51	3.3	19233	4	US-10-204-708-45
C 42	49.4	3.2	665	2	US-08-883-795A-36
C 43	49.2	3.2	64081	4	US-09-790-988-1
C 44	48.4	3.1	832	4	US-09-621-976-2813
C 45	48.4	3.1	3095	6	5231168-1

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/08482037A
; Patent No. 5801028
; GENERAL INFORMATION:
; APPLICANT: Ray Bressan and Paul M. Hasegawa
; TITLE OF INVENTION: Csmotin Gene Promoter and Use Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas Q. Henry
; STREET: Bank One Tower, Suite 3700, 111 Monument Circle
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204-5137
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: COMPAQ
; OPERATING SYSTEM: MSDOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,037A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/476,243
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/180,428
; FILING DATE: January 12, 1994
; APPLICATION NUMBER: 08/065,147
; FILING DATE: May 20, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas Q. Henry
; REGISTRATION NUMBER: 28,309
; REFERENCE/DOCKET NUMBER: 7024-8/PUR16CIPDIVII
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 634-3456
; TELEFAX: (317) 637-7561
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 bases
; TYPE: Nucleotide/Amino Acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: Genomic DNA
US-08-482-037A-1

Query Match 32.3%; Score 500; DB 1; Length 3033;

Best Local Similarity 71.1%; Pred. No. 2.7e-112; Indels 40; Gaps 5;
Matches 749; Conservative 0; Mismatches 265;

Qy 1 ATCTTTGTTTGAATAAATCGTGAAGAACCTAGGACACATGACCTGGTGCACAAAT 60
Db 2619 ATCTTTGTTTGAATAAATCGTGAAGAACCTAGGACACATGACCTGGTGCACAAAT 2560

Qy 61 ATTGTTGCTCTCCAAATGCTGCAAGGATGTTACATCTCCGGGTACTTTAAGCTGAC 120
Db 2559 ATTGTTGCTCTCCAAATGCTGCAAGGATGTTACATCTCCGGGTACTTTAAGCTGAC 2500

Qy 121 TAGGACATTCACCAATTTATTTGCGGTGCAATGAAATGCGTGGCAATTCCTCCCACTTG 180
Db 2499 GGGGACATTCGCGGTGCAATTTAGCGGTGCAATGAAATGCGTGGCAATTCCTCCCACTAG 2440

Qy 181 GATTAGTCGGGGGAAAGTCAATCGGTATATTAATCCATCAACTAAGAAATGCCAGA 240
Db 2439 GATTAGTCGGGGGAAAGTCAATCGGTATATTAATCCATCAACTAAGAAATGCCAGA 2380

Qy 241 AATCTAAGTTGTTGAATGCTCCGAGGCTACTCGGTAGGCTGTTTGGCGGTTTACCCC 300
Db 2379 AATCTAAGTTGTTGAATGCTCCGAGGCTACTCGGTAGGCTGTTTGGCGGTTTACCCC 2320

Qy 301 ACCGGTGCATGACGACACACCAACATCAACAGTCATGACGACGACCTCTACCAAGCAG 360
Db 2319 ACCGGTGCATGACGACACACCAACATCAACAGTCATGACGACGACCTCTACCAAGCAG 2260

Qy 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTAGTCCCTAGGCGCAT 420
Db 2259 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTAGTCCCTAGGCGCAT 2200

Qy 421 CAATGACCCAGTTTGGCTCGATCGAGACGCTCGGCCACCGCTATCGGGGTGCATGCTG 480
Db 2199 TGATCACCCAGTTTGGCTCGATCGAGACGCTCGGCCACCGCTATCGGGGTGCATGCTG 2140

Qy 481 CCCAGACGCTGATGACGACGCTGTTGGTACCTCGATGAGTGGGACGATAGTGAAGTCA 540
Db 2139 CCCAGACGCTGATGACGACGCTGTTGGTACCTCGATGAGTGGGACGATAGTGAAGTCA 2080

Qy 541 CAAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
Db 2079 CCAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2020

Qy 601 ATATGCGGACAAATATTTTGGTACT-----TTATATATAGGAT 641
Db 2019 TTTTAAACAAGTTGGTGTGATATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1960

Qy 642 ATGGCGCTTTTGGCACTATGATTAATTAATCGTATATATAAACAATATCATCTTTGACT 701
Db 1959 ATGGCGCTTTTGGCACTATGATTAATTAATCGTATATATAAACAATATCATCTTTGACT 1905

Qy 702 AATTATAAACAATAATATTAATATGATTTGGTAAACGTTGAGTGGC-AAAATGATAT 760
Db 1904 A--ATAACGATATATCTCAAGGATGCTTTGGCAAGATGAGGCGGCTTAAACAT 1848

Qy 761 AAGAGCGCTTAATAATTAATTTATGAATATAGACTATAGTACAGTGAACCTTAA 820
Db 1847 AAGAGCGCTTAATAATTAATTTATGAATATAG-----AAGTCAATTTA 1800

Qy 821 TTTGGTGATAACTTGGACATATAAATCTGTATCGTGACGGAACCTTTCTTAAACCTAAA 880
Db 1799 TTTGGTGATAACTTGGACATATAAATCTGTATCGTGACGGAACCTTTCTTAAACCTAAA 1740

Qy 881 TATTAAAGACGATTTTAAATATTTTCTGGCCAAAGTTTCTTGCATCTATCTAT 940
Db 1739 AGTCAATTTCTGCTTTCTTTATCTATACCATTTTAAATTCGCAAGAAATGACAGAT 1680

Qy 941 GCCCATTTTCTTTTATCTGTTCTAGCCTTCTAGTACGCTTTGACATATAAATAATCAT 1000
Db 1679 AGCCACTTTTGGCAGATAGCATCAATTTTAAAGCTATTCAATATTAGTTTAAATG 1620

Qy 1001 AAAAATGAAAGTAAATTTAGTTTCTTTTTCATA 1034

Db 1619 AAATAAABAACTCAAAACAATAATATTTCGTCAAAA 1586

RESULT 2
US-07-828-798C-4/c
; Sequence 4, Application US/07828798C
; Patent No. 5389609
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meunelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ladas & Parry
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828, 798C
; FILING DATE: 06-APR-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-8622-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 883
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
US-07-828-798C-4

Query Match 29.1%; Score 450.4; DB 1; Length 883;
Best Local Similarity 85.4%; Pred. No. 2e-100;
Matches 502; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 1 ATCTTTGTTTGAATAAATTTGGAAGAACCTAGGACACATGACCTGGTGCACAAAT 60
Db 602 ATCTTTGTTTGAATAAATTTGGAAGAACCTAGGACACATGACCTGGTGCACAAAT 543

Qy 61 ATTGTTGCTCTCCAAATGCTGCAAGGATGTTACATCTCCGGGTACTTTAAGCTGAC 120
Db 542 ATTGTTGCTCTCCAAATGCTGCAAGGATGTTACATCTCCGGGTACTTTAAGCTGAC 483

Qy 121 TAGGACATTCACCAATTTATTTGCGGTGCAATGAAATGCGTGGCAATTCCTCCCACTTG 180
Db 482 GGGGACATTCGCGGTGCAATTTAGCGGTGCAATGAAATGCGTGGCAATTCCTCCCACTAG 423

Qy 181 GATTAGTCGGGGGAAAGTCAATCGGTATATTAATCCATCAACTAAGAAATGCCAGA 240


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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 883
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-08-315-868A-4

Query Match      29.1%; Score 450.4; DB 2; Length 883;
Best Local Similarity 85.4%; Pred. No. 28-100; Indels 0; Gaps 0;
Matches 502; Conservative 0; Mismatches 86;

QY 1 ATCTTTGTTTGAAGAAATTTGAAAGACGTAGGACCAATGAGGCTTGGGTGCAACAT 60
Db 602 ATCTTTGTTTGAAGAAATTTGAGAAAATGTTAGGACCAACAGGCTCTTGTGTGCAACAT 543
QY 61 ATGTTGTTCTCCAAATGTTGTTACAGGATTTGTTACATCTCTCGGATCTTTAAGTGTAC 120
Db 542 ATGTTGTTCTCCGAAATGTTAGTACAGGGTTTATTACATCTCTCGGAAACCTTAAGTTGCG 483
QY 121 TAGGACATTCACCATTTATATTTGCGTGCAATGAAATGCGTGGCATTTCCCTCCACTTG 180
Db 482 GGGACATTCGCGGTTTATTTAGCGGTACATGAAATGTCATGGCATTTCCCTCCACTAG 423
QY 181 GATTAGTCCGGGCGAAAGTTCATCGGTATATTAATCCATCAATCAAGAAATGTCCAGAC 240
Db 422 GGTAGTCCGGGCGAAAGTTCATCGGAATGTTGAATCCATCAATCAAGAAATGTCCAGAC 363
QY 241 AATCTAAGTTGTTGAATCGTCCGAGGCTACTCGGCTAGGCTGTTTGGCGGTTTACCC 300
Db 362 AATCTAACCCTGAAATGTTGTTCCAAAGCGTATTAGCCAAAGTGTGTTGGTGTGTTTACCC 303
QY 301 ACCCGTGCATGTCAGGACACCAACCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
Db 302 ACCCGTGCATGTCAGGACTCCACCACTGTTGGCGGCTATGCGGCTATGCGGCTGCGAGCG 123
QY 361 CATCGAAGTTACATCCAGTACAGCCCATATACGTGCGATCTAGTGCCTTAGGGCAT 420
Db 242 CATGGAAGTTACATTAATGATAGCGGCCCATACAGTGCATTTTAGTACCTGCTGGCGCAT 183
QY 421 CAATGACCCACCTTTGGCTCTCGATCGAGACGTGCGGCCACCGCTATCGGGTTCGATGCTG 480
Db 182 TGATCACCACCAAGTTTGGCTCTCGATCGAGACGCGGCCACCGCTATGCGGCTGCGAGCG 123
QY 481 CCCAGACGCTGATGACAGTTGTTGGTACCTCGATAGTGCAGCATTAAGTGAAGTCA 540
Db 122 CCCAAACCGGTGACGACAGTTGTTTCGGACCTCGATAGTGCAGCATTAAGTGAAGTCA 63
QY 541 CAAAAGCAAGAGGAGGAGAAACAAAAGAGATCTCAAGTAGCCCATGT 588
Db 62 CCAAGCAAGGAGGAGGAGAAACAAAAGAGATCTCAAGTTGCCCATGT 15

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RESULT 3

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US-08-315-868A-4/c
; Sequence 4, Application US/08315868A
; Patent No. 5856151
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,868A
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APR-1992
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-8622-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 4:

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RESULT 4

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US-08-495-819B-4/c
; Sequence 4, Application US/08495819B
; Patent No. 6037161
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants
; TITLE OF INVENTION: with Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street

```

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PC/XT/AT or compatibles
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/495,819B
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/315,868
FILING DATE: 30-SEPT-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/828,798
FILING DATE: 06-APRIL-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL91/00089
FILING DATE: 31-05-91
ATTORNEY/AGENT INFORMATION:
NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30086
REFERENCE/DOCKET NUMBER: U-010255-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
TELEFAX: (212) 246-8959
TELEX: 233288
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 883
TYPE: Nucleotide
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: Nicotiana tabacum
US-08-495-819B-4

Query Match 29.1%; Score 450.4; DB 3; Length 883;
Best Local Similarity 85.4%; Pred. No. 2e-100;
Matches 502; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1 ATCTTTGTTGAAAAATTTGAAAAAGACGTAGACACACATGACCTTGGTGCAACAT 60
DB 602 ATCTTTGTTGAAAAATTTGAAAAAATGTAGACACACAGGTCTTGTGTGCAACAT 543
QY 61 ATTCTTGTCTCCAAATGTGGTCAAGGATTTATCATCTCTCCGGGTACTTTAAAGCTGAC 120
DB 542 ATTGTGTCTCCGAATGTAGTACAGGTTATTACATCTCTCCGGGAACCTTAAGTTCCG 483
QY 121 TAGACATTCACATTTATATTTGCGGTGCAATGAATTTGGTGGCAATTTCCCTCCACTTG 180
DB 482 GGGGACATTCGCGCGTTTATATTAGCCGTACAAATTTGATGGCATTTCCCTCCACTAG 423
QY 181 GATTAGTCGGGGGAAAGTCATCGGTATATTAAATCCATCACTAAAGAAATGTCACAGA 240
DB 422 GATTAGTCGGGGGAAAGTCATCGGTATATTAAATCCATCACTAAAGAAATGTCACAGA 363
QY 241 AATCTAAGTTGTTGAATCGTCCGAGCGTACTCGGCTAGGTTGTTGGCGGTTTACCCC 300
DB 362 AATCTAAGTTGTTGAATCGTCCGAGCGTACTCGGCTAGGTTGTTGGCGGTTTACCCC 303
QY 301 ACCGGTGCATGACGACACACCAATCAATCAGTCATGACGACCTCTACACAGCAC 360
DB 302 ACCGGTGCATGACGACACCTCCACACAGTCACCGGTTTGGACGACCTCTACACAGCAC 243
QY 361 CATCGAAGTTACATCCAGTACGACCCCATATATCGTGCATCGTAGTCCCTAGGCGCAT 420
DB 242 CATCGAAGTTACATCCAGTACGACCCCATATACATCGTGCATTTAGTACCTCGTGGCGCAT 183

QY 421 CAATGACCCACGTTTGGCTCGATCGAGAGCGTGGCCACCGCCTATCGGGTGTGATCTG 480
DB 182 TGATCACCACCAAGTTTGGCTCGATCGAGAGCGTGGCCACCGCCTATCGGGTGTGACGCG 123
QY 481 CCCAGACGGTGTATGGACAGTTGTTGGTACCTCGATAGTGGCAGCATAAGTGAAGTCA 540
DB 122 CCCAACCGTGTACGGACAGTTGTTTCGGACCTCGATAGTGGCAGCATAAGTGAAGTCA 63
QY 541 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGT 588
DB 62 CCAAGGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTTGCCCATGT 15
RESULT 5
US-07-828-798C-5/c
Sequence 5, Application US/07828798C
Patent No. 5389609
GENERAL INFORMATION:
APPLICANT: Wolessuk, Charles P.
APPLICANT: Melchers, Leo S.
APPLICANT: Cornelissen, Bernardus J. C.
APPLICANT: Meulenhoff, Elisabeth J. S.
APPLICANT: Sela-Buurlage, Marianne B.
APPLICANT: Van Den Elzen, Petrus J. M.
TITLE OF INVENTION: Antifungal Preparations, Process for
TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
TITLE OF INVENTION: Decreased Susceptibility to Fungi
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61st Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PC/XT/AT or compatibles
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/NL91/00089
FILING DATE: 31-05-91
ATTORNEY/AGENT INFORMATION:
NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30086
REFERENCE/DOCKET NUMBER: U-8622-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
TELEFAX: (212) 246-8959
TELEX: 233288
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 884
TYPE: Nucleotide
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: Nicotiana tabacum
US-07-828-798C-5

Query Match 29.1%; Score 450.4; DB 1; Length 884;
Best Local Similarity 85.4%; Pred. No. 2e-100;
Matches 502; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1 ATCTTTGTTGAAAAATTTGAAAAAGACGTAGACACACATGACCTTGGTGCAACAT 60
DB 602 ATCTTTGTTGAAAAATTTGAAAAAATGTAGACACACAGGTCTTGTGTGCAACAT 543

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QY 61 ATTGTTCTCTCCAAATGTGGTACAAGATGTTTACATCTCCGGGPACTTTAAGTGC 120
DB 542 ATTGTTCTCTCCAAATGTGGTACAAGATGTTTACATCTCCGGGPACTTTAAGTGC 483
QY 121 TAGGACATTCACCAATTTATTTGCGTGCATTAAGTGGTGGTGGTGGTGGTGG 180
DB 482 GGGGACATTCACCAATTTATTTAGCGGTACAAATGATGATGATGATGATGATG 423
QY 181 GATTAGTCGGGGGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAAATGCC 240
DB 422 GGTAGTCGGGGGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAAATGCC 363
QY 241 AATCTAGTTGTTGAACTGTCGAGGCTACTCGGTAGGGTGGTGGTGGTGGTGG 300
DB 362 AATCTAGTTGTTGAACTGTCGAGGCTACTCGGTAGGGTGGTGGTGGTGGTGG 303
QY 301 ACCGGTGCATTCAGGACACCAACATCACAGTCAATCGGTAGGGTGGTGGTGG 360
DB 302 ACCGGTGCATTCAGGACACCAACATCACAGTCAATCGGTAGGGTGGTGGTGG 243
QY 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTACGACCCCAT 420
DB 242 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTACGACCCCAT 183
QY 421 CAATGACCCAGTTGTCGCTCGATCGAGAGCGTGGCCACCGCTATCGGGGTG 480
DB 182 TGATCACCAGTTGTCGCTCGATCGAGAGCGTGGCCACCGCTATCGGGGTG 123
QY 481 CCCAGACGGTGTATGACAGTGTGTCGTCATCGATAGTGGCAGCATTAAGTCA 540
DB 122 CCCAAACGGTGTATGACAGTGTGTCGTCATCGATAGTGGCAGCATTAAGTCA 63
QY 541 CAAAGCAAGAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATGT 588
DB 62 CCAAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15

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RESULT 6
US-08-315-868A-5/C
; Sequence 5, Application US/08315868A
; Patent No. 5856151
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buiriage, Marianne B.
; APPLICANT: Van Den Eizen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315, 868A
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828, 798
; FILING DATE: 06-APR-1992
; APPLICATION NUMBER: PCT/NL91/00089

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; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-8622-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-08-315-868A-5

Query Match 29.1%; Score 450.4; DB 2; Length 884;
Best Local Similarity 85.4%; Pred. No. 2e-100;
Matches 502; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1 ATCTTTGTTGAAAAAATTGAAAAAAGCGTAGGACCAATGGACCTTGGGGTGCACCAAT 60
DB 602 ATCTTTGTTGAAAAAATTGAAAAAAGCGTAGGACCAATGGACCTTGGGGTGCACCAAT 543
QY 61 ATTGTGTCCTCCAAATGTGGTACAAGGATGTTTACATCTCTCCGGGTACTTTAAGTGC 120
DB 542 ATTGTGTCCTCCAAATGTGGTACAAGGATGTTTACATCTCTCCGGGTACTTTAAGTGC 483
QY 121 TAGGACATTCACCAATTTATTTGCGTGCATTAAGTGGTGGTGGTGGTGGTGG 180
DB 482 GGGGACATTCACCAATTTATTTAGCGGTACAAATGATGATGATGATGATGATG 423
QY 181 GATTAGTCGGGGGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAAATGCC 240
DB 422 GGTAGTCGGGGGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAAATGCC 363
QY 241 AATCTAGTTGTTGAACTGTCGAGGCTACTCGGTAGGGTGGTGGTGGTGGTGG 300
DB 362 AATCTAGTTGTTGAACTGTCGAGGCTACTCGGTAGGGTGGTGGTGGTGGTGG 303
QY 301 ACCGGTGCATTCAGGACACCAACATCACAGTCAATCGGTAGGGTGGTGGTGG 360
DB 302 ACCGGTGCATTCAGGACACCAACATCACAGTCAATCGGTAGGGTGGTGGTGG 243
QY 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTACGACCCCAT 420
DB 242 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTACGACCCCAT 183
QY 421 CAATGACCCAGTTGTCGCTCGATCGAGAGCGTGGCCACCGCTATCGGGGTG 480
DB 182 TGATCACCAGTTGTCGCTCGATCGAGAGCGTGGCCACCGCTATCGGGGTG 123
QY 481 CCCAGACGGTGTATGACAGTGTGTCGTCATCGATAGTGGCAGCATTAAGTCA 540
DB 122 CCCAAACGGTGTATGACAGTGTGTCGTCATCGATAGTGGCAGCATTAAGTCA 63
QY 541 CAAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 588
DB 62 CCAAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15

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RESULT 7
US-08-495-819B-5/C
; Sequence 5, Application US/08495819B
; Patent No. 6087161
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.

```

APPLICANT: Meulenhoff, Elisabeth J. S.
 APPLICANT: Sela-Buurlage, Marianne B.
 APPLICANT: Van Den Elzen, Petrus J. M.
 TITLE OF INVENTION: Antifungal Preparations, Process for
 TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants
 TITLE OF INVENTION: With Decreased Susceptibility to Fungi
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ladas & Parry
 STREET: 26 West 61st Street
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10023
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
 COMPUTER: IBM PC/XT/AT or compatibles
 OPERATING SYSTEM: DOS
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/495,819B
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/315,868
 FILING DATE: 30-SEPT-94
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/828,798
 FILING DATE: 06-APRIL-92
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/NL91/00089
 FILING DATE: 31-05-91
 ATTORNEY/AGENT INFORMATION:
 NAME: Mass, Clifford J.
 REGISTRATION NUMBER: 30086
 REFERENCE/DOCKET NUMBER: U-010255-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 708-1800
 TELEFAX: (212) 246-8959
 TELEX: 233288
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 884
 TYPE: Nucleotide
 STRANDEDNESS: Double
 TOPOLOGY: Linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Nicotiana tabacum
 US-08-495-819B-5

Query Match 29.1%; Score 450.4; DB 3; Length 884;
 Best Local Similarity 85.4%; Pred. No. 2e-100;
 Matches 502; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1 ATCTTTGTTTGAAGAAATTCGAAAGAACCTAGGACCACTGACCTGGGTGCAACAAAT 60
 DB 602 ATCTTTGTTTGAAGAAATTCGAAAGAACCTAGGACCACTGACCTGGGTGCAACAAAT 543

QY 61 ATTGTTGTCCTCCAAATGTGGTCAAGGATGTGATCATCTCCGGGTACTTTAAGCTGAC 120
 DB 542 ATTGTTGTCCTCCAAATGTGGTCAAGGATGTGATCATCTCCGGGTACTTTAAGCTGAC 483

QY 121 TAGGACATTCACCAATTTATATTTGCGGTGATGAAATTCGCTGGCAATTTCCCTCCACTTG 180
 DB 482 GGGGACATTCGCGTTTATATTAGCGGTACATGAAATTCGATGCGCAATTTCCCTCCACTTG 423

QY 181 GATTAGTCGGGGCGAAAGTCAATCGGTATATTAATCCATCACTAAAGAAATGTCCAGA 240
 DB 422 GGTAGTCGGGGCGAAAGTCAATCGGTATATTAATCCATCACTAAAGAAATGTCCAGA 363

QY 241 AATCTAAGTTGTTGAATGTCGCGGTACTCGGCTAGGTTGTTGGGGTTTACCCC 300

Db 362 AATCTAAGTTGTTGAATGTCGCGGTACTCGGCTAGGTTGTTGGGGTTTACCCC 303
 QY 301 ACCGGTGCACCTGAGGACACCAACCAATCAGGATCATGACGAACTCTACCGAC 360
 Db 302 ACCGGTGCACCTGAGGACACCAACCAATCAGGATCATGACGAACTCTACCGAC 243
 QY 361 CATGGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCTAGTCCCTTAGGGCAT 420
 Db 242 CATTGAAGTTTAAATTTAGTACGGCCCCCATACAGTGCCATTTTAGTACCTCGTGGCGCAT 183
 QY 421 CAATGACCCACGTTTGGCTTCGATCGAGAGCGTGGCCACCGCTATCGGGGTGATGCTG 480
 Db 182 TGATCACCCCAAGTTTGGCTTCGATCGAGAGCGCGGCCACCGCTATCGGGGTGATGCTG 123
 QY 481 CCCAGACGCTGTATGGACAGTTGTTGGCTACCTCGATAGTGGGACATTAAGTGAAGTCA 540
 Db 122 CCCAAACGGTGTACGGACAGTTGTTGGACCTCGATAGTGGGACATTAAGTGAAGTCA 63
 QY 541 CAAAGCAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGGCCCATGT 588
 Db 62 CCAAGGCAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGGCCCATGT 15

RESULT 8
 US-09-589-733C-4/c
 ; Sequence 4, Application US/09589733C
 ; Patent No. 6677503
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Crasta, Oswald R.
 ; APPLICANT: Duwick, Jon
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guihua
 ; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
 ; TITLE OF INVENTION: Genes and their Uses
 ; FILE REFERENCE: 5718-90
 ; CURRENT APPLICATION NUMBER: US/09/589,733C
 ; PRIOR FILING DATE: 2000-06-08
 ; PRIOR APPLICATION NUMBER: 60/140,646
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/162,904
 ; PRIOR FILING DATE: 1999-11-01
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 875
 ; TYPE: DNA
 ; ORGANISM: Helianthus annuus
 US-09-589-733C-4

Query Match 11.7%; Score 180.6; DB 4; Length 875;
 Best Local Similarity 60.9%; Pred. No. 1e-34;
 Matches 332; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

QY 1 ATCTTTGTTTGAAGAAATTCGAAAGAACCTAGGACCACTGACCTGGGTGCAACAAAT 60
 DB 577 ATCTTTGTTTGAAGAAATTCGAAAGAACCTAGGACCACTGACCTGGGTGCAACAAAT 518

QY 61 ATTGTTGTCCTCCAAATGTGGTCAAGGATGTGATCATCTCCGGGTACTTTAAGCTGAC 120
 DB 517 ACTGATCAGTTTGTACACGGTGCAGGGTTATTGACCCCGCAGGAGCCGTAACCTAC 458

QY 121 TAGGACATTCACCAATTTATATTTGCGGTGATGAAATTCGCTGGCAATTTCCCTCCACTTG 180
 DB 457 CAGGACATTCGCAATTCATATCCGACGTACATGAGATACCCCGGTGCACCC-----AT 404

QY 181 GATTAGTCGGGGCGAAAGTCAATCGGTATATTAATCCATCACTAAAGAAATGTCCAGA 240
 DB 403 TAGAATTTGGTCTAAACACCATCGGCATTTGAATCCGCTCCCAAGAGAAATGTCAAGA 344

QY 241 AATCTAAGTTGTTGAATGTCGCGGTACTCGGCTAGGTTGTTGGGGTTTACCCC 300
 DB 343 AATCTAAGTTGTTGAATGTCGCGGTACTCGGCTAGGTTGTTGGGGTTTACCCC 284

QY 301 ACCGGTCACTGAGGACACCAACCAATCACCAGTCAATGACGAACTTACCAGCAC 360
Db 283 AGTTTGGCATTTGGAGGAGACCGTTGCAATCACCGGCTGACACTGCTCGCCGCAAC 224
QY 361 CATGAAGTTATCATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCTAGCGCGCAT 420
Db 223 CATCAAGTTGCAATTTGGTTCGGGSCCATATACGGGCTCCTGCTGTCAGCTCGGACGG 164
QY 421 CAATGACCCAGTTTGGCTCGATCGAGACGTCGGCCACCGCTATCGGGTCCATGCTG 480
Db 163 TTAAGACCGATTGGCTGAGTTAAGTTGTCGGCGCCACC--AGGCACCCACACAG 107
QY 481 CCCGACCGTGTATGACGAGTGTGTCGTCTCATATAGTGGCAGCATAAAGTCA 540
Db 106 CCCAACCGTGTATGACGAGTGTTCGAATAGTGAACCGCTGCAATGATATAGTGA 47
QY 541 CAJAA 545
Db 46 AAAGA 42

RESULT 9
US-08-181-271A-4/c
; Sequence 4, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/Pl/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-181-271A-4

Query Match 10.3%; Score 159.2; DB 1; Length 900;
Best Local Similarity 61.1%; Pred. No. 1.7e-29;
Matches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;
QY 1 ATCTTTGTTTGAAGAAATGGAAGACGCTAGGACCCACAT-----GGACCTTGGGTGC 54
Db 604 ATCTTTCCTTAAATAATCTCGACAATCAGTAGGCCACATGATCCAGGCCCATTTGTAC 545
QY 55 AACAAATATTGTTGCTCCTCCAAATGTTGTTCAAGATTGTTACATCTCCGGGTACTTTAA 114
Db 544 AACAAATATTGTTGCTCCTCCAAATGTTGTTCAAGATTGTTACATCCACCTTGTGTTTCA 485
QY 115 GCTGACTAGGACATTCAACCATTTATATTGTCGTCGTCATTGAATTGCGTGGCATTTCCCTC 174
Db 484 ACTGTGCTGGGCATTGTTGCTTAAATAGTGTGTCGATCTGAGATTACGACATCTCTCC-- 427
QY 175 CACTTGGATTAGTCGGGGCGGAAAGTCATCGGTPATATTAAATCCATCAACTAAAGAAATG 234
Db 426 -----ATTGTCGGGCTGAATTCATGGGGATGTTAAATCCATCAACAGAGAGATGT 374
QY 235 CCCAGAAATCTAAGTTGTTGAACTGGTCCGAGCGCTACTCGGCTAGGGTGTGGGGTT 294
Db 373 CGACAAAGTC---CTGATTGGGTTGATTAAAGTCAAAATTCAGCTAAAGTTAGGTGCTT 317
QY 295 TACCCCAACCCGGTGCATCTGACGAGCACCACCAACATCAGCTCATGACGACAACTCTAC 354

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316 TTCATAGCTTGCATCTTACATCCGTTACAGTCTCAGTCTCACAATACCTCGGC 257
355 CAGCAGCATGAGTACATCCAGTACGAGCCCATATACGTGCTAGTGCCTTAG 414
256 CACTGCCATGAGTGTCAATTTGTTCCGACCCCAATGCGAGCTGTTCTCTGGGT 197
415 GCGCATCAATGACCCAGTGTGGCTCGATCGAGAGTGGCCACCGCTATCGGGTGC 474
196 TCACATTAATGCTCAAGATTGGCTGAGTCGAGCCGCTGCTCCACCT---GGAGAG 140
475 ATGTGCGCCAGAGCGGTGTATGACAGTGTGTGGTACCTCGATGAGCGCAGCATAAGTGA 534
139 CCGCGGCCAGACTGTGTAGTGTGCAATTTGTTGACAATGTCAAAAGTGGCAGCATGAGTAA 80
535 AAGTCACAAA 544
79 CAGCTACAAA 70

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RESULT 10

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US-08-449-315-4/c
; Sequence 4, Application US/08449315
; Patent No. 5650505
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESS: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,315
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/532,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-449-315-4
; Query Match 10.3%; Score 159.2; DB 1; Length 900;
; Best Local Similarity 61.1%; Pred. No. 1.7e-29;
; Matches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;
QY 1 ATCTTTGTTGAAAAAATGGAAAAAGACGTAGACCAATF-----GGACCTTGGGTGC 54
Db 604 ATCTTTCTTAAAAAATCTCGACAAATCAGTAGGCCCAATGATCCAGGCCCAATTTGTAC 545
QY 55 AACAAATATTGTTGCTCCCAATGTGGTACAGGATTGTTACATCTCCCGGTACTTTAA 114
Db 544 AACAAATATTGTTGTTTATTCACAGTACATGGTGTGTTACATCCACCTTGTGTTTCA 485
QY 115 GCTGACTAGGACATTCACCAATTTATTTTTCGCGGCGGTACTCGGCTAGGGTGTTCCTC 174
Db 484 ACTGTGCTGGGCAITGTTGTTTAAATAGTGTGTCATCTGAGATTACGACATCCTCC-- 427
QY 175 CACTTGGATTAGTCGGGGCGAAGTCACTCGTATATTAAATCCATCACTAAAGAAATGT 234
Db 426 -----ATTGTCGGGCTGAATTCCTATGGGATGTTAAATCCATCAACAGAGAGTGT 374
QY 235 CCCAGAAATCTAAGTGTGTGAACCTGGTCCGAGGCGGTACTCGGCTAGGGTGTTCGGCGGTT 294
Db 373 CGACAAAGTCT---CTGATTGGGTTGATTAAAGTCAAAATTCAGCTAAAGTGTAGGTGCTT 317
QY 295 TACCCACCCCGGTGCTGAGGACACCAACCAATCACCAGTCATGCACGACCTCTAC 354

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Db      316  TTCCATACGCTTGACACTCTAACATCCCGTTACAGTCTCCAGTCTCAAAATTACCTCGGC 257
Qy      355  CAGCACCATCAAGTTACATCCAGTAGCAGACCCCATATACGTGCCATCGTAGTCCCTAG 414
Db      256  CACTGCCATCAAGTTGCAATTGGTTCGACCCCAATCGGAGCTCGACTGTTCTCGGT 197
Qy      415  CGGATCAATGACCCAGCTTTGGCTCGATCGAGAGCTCGGCCACCGCCTATCGGGTCG 474
Db      196  TCACATTAATGCTCCAAGATTGGCTGAGTCGAGCGCGCTGCCCTCCACCT---GGAGAGG 140
Qy      475  ATGTGCCACGACGCTGTATGACAGTGTGTGCGTACCTCGATAGTGGCAGCATAAGTGA 534
Db      139  CCGCGGCCGACACTGTGTAGTGTGATTTGTGACAATGTCAAAAGTGGCAGCATGACTAA 80
Qy      535  AAGTCACAAA 544
Db      79  CAGCTACAAA 70

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RESULT 11

US-08-444-803-4/c
 ; Sequence 4, Application US/08444803
 ; Patent No. 5654414

GENERAL INFORMATION:

; APPLICANT: Ryals, John A.
 ; APPLICANT: Alexander, Danny C.
 ; APPLICANT: Beck, James J.
 ; APPLICANT: Duesing, John H.
 ; APPLICANT: Friedrich, Leslie B.
 ; APPLICANT: Goodman, Robert M.
 ; APPLICANT: Harms, Christian
 ; APPLICANT: Meins, Jr., Frederick
 ; APPLICANT: Montoya, Alice
 ; APPLICANT: Moyer, Mary B.
 ; APPLICANT: Neuhaus, Jean-Marc
 ; APPLICANT: Payne, George B.
 ; APPLICANT: Sperison, Christoph
 ; APPLICANT: Stinson, Jeffrey R.
 ; APPLICANT: Uknes, Scott J.
 ; APPLICANT: Ward, Eric R.
 ; APPLICANT: Williams, Shericca C.
 ; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 ; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CIBA-GEIGY Corporation
 ; STREET: 7 Skyline Drive
 ; CITY: Hawthorne
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10532

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,803
 ; FILING DATE: 19-MAY-1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/181,271
 ; FILING DATE: 13-JAN-94
 ; APPLICATION NUMBER: US 08/093,301
 ; FILING DATE: 16-JUL-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/937,197
 ; FILING DATE: 6-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/678,378
 ; FILING DATE: 1-APR-1991
 ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566
 ; FILING DATE: 6-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/165,667
 ; FILING DATE: 8-MAR-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/042,847
 ; FILING DATE: 6-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/632,441
 ; FILING DATE: 21-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/425,504
 ; FILING DATE: 20-OCT 1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/848,506
 ; FILING DATE: 6-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/768,122
 ; FILING DATE: 27-SEP-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/580,431
 ; FILING DATE: 7-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/368,672
 ; FILING DATE: 20-JUN-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/329,018
 ; FILING DATE: 24-MAR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/045,957
 ; FILING DATE: 12-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Elmer, James Scott
 ; REGISTRATION NUMBER: 36,129
 ; REFERENCE/DOCKET NUMBER: S-19825/Pl/CGC 1727
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919)541-8614
 ; TELEFAX: (919)541-8689
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 900 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; US-08-444-803-4

Query Match 10.3%; Score 159.2; DB 1; Length 900;

Best Local Similarity 61.1%; Pred. No. 1.7e-29;
 Matches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;

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Qy      1  ATCTTTGTTTGAATAAATTGAAAGAACGTAGGACCACAT-----GGACCTTGGGTGC 54
Db      604  ATCTTTCTTTAAATAATCTCGCAATCAGTAGGCCACATGATCCAGGCCCATTTGTAC 545
Qy      55  AACAAATATTGTTGCTCTCCAAATGTGGTACAGGATGTATCATCTCCGGGTACTTTAA 114
Db      544  AACATATATTCAATTGGTTTATATACAGTACATGGGTGTGTATACATCCACCTTGTGTTTCA 485
Qy      115  GCTGACTAGGACATTCACCATTTATATTTGCGGTGCATTGAATTTGGTGGCATTTCCCTC 174
Db      484  ACTGTCTGGGCATTTGTTGTTAATAGGTGTGTGCACTGAGATTACACATCTCTCC-- 427
Qy      175  CACTTGGATTAGTCGGGGCGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAAATGT 234
Db      426  -----ATTGTCGGGCTGAATTTCCATGGGATGTTAAATCCATCAACAAGAGATGT 374
Qy      235  CCAGAAATCTAAGTTGTTGAAGTGTGCTCGAGCGGTACTCGGTAGGTGTTTGGCGGTT 294
Db      373  CGACAAAGTC---CTGAATTGGGTGTTAATTAAGTGCATAAATTCAGCTAAAGTTGTAGGTGCTT 317
Qy      295  TACCCCAACCCGGTGCACTGCAGGACACACCACCAATCACCAGTCATGCACGAACCTCTAC 354

```

Db 316 TTCCATAGCTTGACACTTAACATCCCGTTTACAGTCTCCAGTCTCACAATTACCTCGGC 257
QY 355 CAGCACCATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCTTAG 414
Db 256 CACTGCCATCGAAGTTGCAATGTTGACCCCAATGCGAGCCTGAGACTGTTCTTGGGT 197
QY 415 GCGCATCAATGACCCAGCTTTGGCTCGATGAGACGTGCGCCACCCCTTATCGGGTGC 474
Db 196 TCATTAAATGCTCAAAGTTGGCTGAGTCGAGCCGCTGCTCCACCT--GGAGAGG 140
QY 475 ATGCTGCCAGACCGTGTAGGACAGTGTGCTACTCTGATAGTGGCAGCATAGTGA 534
Db 139 CCGGGGCCAGACTGTGTAGTGCATTTGTTGCAATGTCAAAAGTGGCAGCATGAGTAA 80
QY 535 AAGTCACAAA 544
Db 79 CAGCTACAAA 70

RESULT 12

US-08-449-043-4/c
; Sequence 4, Application US/08449043
; Patent No. 5689044

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-449-043-4

Query Match 10.3%; Score 159.2; DB 1; Length 900;

Best Local Similarity 61.1%; Pred.No.1.7e-29;

Matches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;

QY 1 ATCTTTGTTTGAAGAAATGGAAGAACGTAGACCCACAT-----GGACCTTGGGTGC 54
Db 604 ATCTTCTCTTAAATAATCTCGACAAATCAGTAGGCCACATGATCCAGGCCCATTTGTAC 545
QY 55 AACCAATATTGTTGCTCCCAATGTGTACAAAGATTGTTACATCTCCGGGTACTTTAA 114
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Db 484 ACTGTGCTGGGCATTGTTTCGTTAATAGTGTGTCGATCTGAGATTACGACATCCCTCC-- 427
QY 175 CACTTGGATTAGTCGGCGGCAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGT 234
Db 426 -----ATTGTCGGGCTGNAATTCATGGGATGTTAATTCATCAACAAGAGATGT 374
QY 235 CCCAGAAATCTAAGTTGTTGAACTGCGGTCCGAGGCGTACTCGGTAGGGTGTGTTGGCGGTT 294
Db 373 CGACAAAGTC---CTGATTGGGTTGATTAAAGTGCAAATTCAGCTAAAGTGTAGTGCTT 317
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Db 139 CCGGGCCCACTGTGTAGTGCATTGTTGACAAATGTCAAAGTGGCAGCATGAGTAA 80
QY 535 AAGTCACAAA 544
Db 79 CAGCTACAAA 70

RESULT 14
US-08-455-416-4/c
; Sequence 4, Application US/08455416
; Patent No. 577200
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericea C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,416
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-455-416-4

Query Match 10.3%; Score 159.2; DB 1; Length 900;
Best Local Similarity 61.1%; Pred. No. 1.7e-29;
Matches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;

QY 1 ATCTTTGTTTCAAAAAATTTGAAAAAGACGTAGGACACACAT-----GGACCTTGGGTGC 54
Db 604 ATCTTTCTTTAAAAATCTCGAATAATCAGTAGGCCACATGATCCAGGCCAATTTGTAC 545
QY 55 AACAAATATTGTGTCCTCCAAATGTGTACAAAGATTGTGTACATCTCTCCGGGTACTTTAA 114
Db 544 AACAAATATTCTGTTTATTCACAGTACATGGGTGTTTACATCCACCTGTGTTTCA 485
QY 115 GCTGACTAGGACATTCACCATTTATTTTCGCGTGCATTGAAATTGCGTGGCATTTCCCTC 174
Db 484 ACTGTGCTGGGCATTGTTTCGTTAATAGTGTCTGCACTCTGAGATTACGACATCCTCC-- 427
QY 175 CACTTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAAATATTAATCCATCAACTAAAGAAATGT 234
Db 426 -----ATTGTCGGGCTGAATTCATGGGATGTTAAATCCATCAACAAGAGATGT 374
QY 235 CCCAGAAATCTAAGTTGTTGAACTGGTCCGAGGGGTACTCGGCTAGGGTGTGGCGGTT 294
Db 373 CGACAAAGTC---CTGATTGGGTTGATTAAAGTGCAAAATTCAGCTTAAAGTGTAGGTGCTT 317
QY 295 TACCCCAACCCGGTGCATCTGCAGGACACACACCAATCACAGTCAATCGACGAACCTCTAC 354
Db 316 TTCCATAGCCTTGACACTCTAACATCCGGTTACAGTCTCCAGTCTCACATTACCTCGGC 257
QY 355 CAGCACATCGAAGTTACATCCAGTACGACCCCATATACGTGTCATCGTAGTGTAGTCCCTAG 414
Db 256 CACTGCCATCGAAGTTGCAATTTGTTTCGACCCCAATTCGAGCGCTGGAAGTGTCTCTGGGT 197
QY 415 GCGCATCAATGACCCACGTTTGGGCTCGATCGAGACGCTCGGCCACCGCCTATCGGGGTG 474
Db 196 TCACATTAAATGCTCCAAGATTGGCTGAGTCGAGCGCCTGCTCCACCT---GGAGAGG 140
QY 475 ATGTGCCAGACGGTGTATGGACAGATTGTTGGGTACCTCGATAGTGGCAGCATAGTGA 534

Db 139 CCGCGGCCAGACGTGTAGTGTGATTTGTTGACAAATGTCAAAAGTGGCAGCATGAGTAA 80
QY 535 AAGTCACAAA 544
Db 79 CAGCTACAAA 70

RESULT 15

US-08-455-244-4/c.
Sequence 4, Application US/08455244
Patent No. 5789214
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
APPLICATION NUMBER: US 07/678,378
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
APPLICATION NUMBER: US 07/165,667
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
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APPLICATION NUMBER: US 07/632,441
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APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
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APPLICATION NUMBER: US 07/368,672
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/Pl/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-455-244-4

Query Match 10.3%; Score 159.2; DB 1; Length 900;
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QY 1 ATCTTTGTTTGAATAATTCGAAAGACAGTAGGACCAAT-----GGACCTTGGGTGC 54
Db 604 ATCTTTCTTAAAAATCTCGACAAATCAGTAGGCCCCACATGATCCAGGCCCATTTGTAC 545
QY 55 AACAATATTTGTTCTCTCCAAATGTTGTTACAGGATTTTACATCTCCGGGTACTTTAA 114
Db 544 AACAATATTTGTTCTCTCCAAATGTTGTTACAGGATTTTACATCTCCGGGTACTTTAA 485
QY 115 GCTGACTAGGACATTCACCAATTTATATTTGCGGTGCAATTCGTTGGCATTTCCCTC 174
Db 484 ACTGTCTGGCATTTGTTGTTAAATAGGTGCTGTGATCTGAGATTACGACATCCCTCC-- 427
QY 175 CACTTGGATTAGTCGGGGGAAAGTCACTCGGTATATTAATTCATCACTAAGAATGT 234
Db 426 -----ATTGTCGGGCTGAATTCATCGGGATGTTAAATCCATCAACAGAGAGATGT 374
QY 235 CCGAGAAATCTAAGTTGTTGAACTGCTCGAGGCGTACTCGGCTAGGTGTTTGGCGGTT 294
Db 373 CGACAAAGTC---CTGATTTGGGTTGATTAAGTGCATTTTACGTTAAGTTAGGTGCTT 317
QY 295 TACCCCAACCGGTGCACTCGAGGACACCAACAATCAACAGTCATGACAGCACTCTAC 354
Db 316 TTCCATAGGCTTGACACTCTAACATCCCGTTACAGTCTCAGTCTCACAATTTACCTCGGC 257
QY 355 CAGCACCATCGAGTTTACATCCAGTACGACCCCATATAGTCATCGTAGTGCCTTAG 414
Db 256 CACTGCCATCGAAGTTGCAATTTGGTTTCGACCCCAAAATGAGGCTCGATGTTCTTGGGT 197
QY 415 GCGCATCAATGACCCACGTTTGGCTTCGATCGAGAGCTCGGCCACCGCTTATCGGGGTG 474
Db 196 TCACATTAATGCTCCAAAGTTGSCCTGAGTGGAGCGGCTGCTCCACCT---GGAGAGG 140
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Qy	535	AAATCACAAA	544
Db	79	CAGCTACAAA	70

Search completed: August 18, 2004, 16:17:40
 Job time : 122.074 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 03:35:10 ; Search time 5856.14 Seconds
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Title: US-10-051-307-3
Perfect score: 1546
Sequence: 1 atctttgttgaaaaaatg.....tggtgaagttggtgtttc 1546

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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C 5	563.6	36.5	2638	8	SC13OLP	S.commerson
C 6	550.4	35.6	1304	8	AF093743	Lycopersi
C 7	508	32.9	301	8	SC08MLP	S.commerson
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C 15	467.6	30.2	818	8	AY007309	Solanum d
C 16	467.6	30.2	937	8	AF297646	Capsicum
C 17	465.4	30.1	856	8	CAN297410	Sequence
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C 21	450.4	29.1	883	6	AR103205	Sequence
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C 31	443	28.7	917	8	TOMNP24	Tomato NP24
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C 40	416.6	26.9	538	8	AY256430	Solanum t
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C 44	407.8	26.4	541	8	AY256428	Solanum t
C 45	406.6	26.3	542	8	AY256437	Solanum t

ALIGNMENTS

RESULT 1
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LOCUS AX665980 1546 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 3 from Patent WO02059333.
ACCESSION AX665980
VERSION AX665980.1 GI:29290849
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
AUTHORS Dai, Z., Shi, L. and Hooker, B.S.
TITLE Gene promoters isolated from potato and use thereof

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 02059333-A 3 01-AUG-2002;
Dai, Ziyu (US); Shi, Lifang (US); Hooker, Brian, S. (US)

FEATURES
Location/Qualifiers
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/organism="Solanum tuberosum"
/mol_type="unassigned DNA"
/db_xref="taxon:4113"

ORIGIN

Query Match 99.9%; Score 1545; DB 6; Length 1546;
Best Local Similarity 100.0%; Pred. No. 4.2e-302; Indels 0; Gaps 0;
Matches 1546; Conservative 0; Mismatches 0;

QY 1 ATCTTTGTTGAAAAAATGGAAAGAACGTAGGACCAATGGGTCACAAT 60
DB 1 ATCTTTGTTGAAAAAATGGAAAGAACGTAGGACCAATGGGTCACAAT 60
QY 61 ATTGTTGTCCTCCAAATCGGTACAGGATGTTACATCTCCGGTACTTTAAGCTGAC 120
DB 61 ATTGTTGTCCTCCAAATCGGTACAGGATGTTACATCTCCGGTACTTTAAGCTGAC 120
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DB 121 TAGGACATTCACCAATTTATATTTGCCGTGCAATGAAATGGCGTCAATTCCTCCACTTG 180
QY 181 GATTAGTCGGGGCGGAAAGTCATCGGTATATTTAAATCCATCAATCAAAAGAAATGTCCAGA 240
DB 181 GATTAGTCGGGGCGGAAAGTCATCGGTATATTTAAATCCATCAATCAAAAGAAATGTCCAGA 240
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DB 241 AATCTAAGTCTGTGAATGGTCCGAGCGGTACTCGGTAGGCTGTTGGCGGTTTACCCC 300
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DB 301 ACCGGTGCATCGAGGACACCAACAATCAGTCATCGACGAACCTCTACCCAGCAC 360
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QY 961 TTCTAGCCTTCTAGGTACGCGTTTGAAACATAAAAAATCATAAAAATGAAAGTAAAAAT 1020
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DB 1081 ATTCTGATTTTAAAAATCATAACTATTTGCTATGATGGGAACGTCTATGCTGATTCGTGAC 1140
QY 1141 AAGTGTGTTGATTTATCTAAGTCTCGATGAGTCAAACTTTTGTAGTGCATAATCTATT 1200
DB 1141 AAGTGTGTTGATTTATCTAAGTCTCGATGAGTCAAACTTTTGTAGTGCATAATCTATT 1200
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QY 1261 TTACGATCGGAGCATGGATACATTTACTAATTAATAAATTTGGAAGAAATGATCGACA 1320
DB 1261 TTACGATCGGAGCATGGATACATTTACTAATTAATAAATTTGGAAGAAATGATCGACA 1320
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DB 1441 TCTAAACTAATGATCATCTACACACAAATATAAATCTAGATCTTTTAAAGAAATGCA 1500
QY 1501 GAATTAATGAGGCAAAATAGTCTATGTTGAAAGTTGGTCTCTTTC 1546
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RESULT 2

AX665978
LOCUS AX665978 1595 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1 from Patent WO02059333.
ACCESSION AX665978
VERSION AX665978.1 GI:29290847

KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum

REFERENCE 1 Dai, Z., Shi, L. and Hooker, B.S.
AUTHORS Gene promoters isolated from potato and use thereof
TITLE Patent: WO 02059333-A 1 01-AUG-2002;
JOURNAL Dai, Ziyu (US); Shi, Lifang (US); Hooker, Brian, S. (US)

FEATURES

Location/Qualifiers
1. 1595
/organism="Solanum tuberosum"
/mol_type="unassigned DNA"
/db_xref="taxon:4113"

ORIGIN

Query Match 88.1%; Score 1362.4; DB 6; Length 1595;
Best Local Similarity 94.1%; Pred. No. 3.4e-265;
Matches 1460; Conservative 0; Mismatches 82; Indels 9; Gaps 4;

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Db	49	ATCTTTGTTGAAAAATTTGAAAGAACGTTAGGACCAATGGACCTTGGTGCACAAAT	108
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Db	109	ATTGTGTCCTCCAAATGTTGTAAGAAATGTTTACATCCTCCGGGTAATTTAAGTTGAC	168
QY	121	TAGGACATTCACCAATTTATTTTCCGTCGATGAAATGCGTGGCAATTTCCCTCCACTTG	180
Db	169	CAGGCAATTCACCAATTTATTTTCCGTCGATGAAATGCGTGGCAATTTCCCTCCACTTG	228
QY	181	GATTAGTCGGGGGAAAGTCAATCGGTATTTAAATCCATCAACTTAAAGAAATGTCACAGA	240
Db	229	GATTAGTCGGGGGAAAGTCAATCGGTATTTAAATCCATCAACTTAAAGAAATGTCACAGA	288
QY	241	AATCTAAGTTGTTGAACTCGTCCGAGGCTACTCGGCTAGGCTGTTTGGCGGTTTACCC	300
Db	289	AATCTAAGTTGTTGAACTCGTCCGAGGCTACTCGGCTAGGCTGTTTGGTGGTTGCCCC	348
QY	301	ACCGGTGTCAGTCGAGGACACCAATCAACAGTCAATGACGAACTCTACACGAC	360
Db	349	ACCGGTGTCAGTCGAGGACACCAATCAACAGTCAATGACGAACTCTACACGAC	408
QY	361	CATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCGTAGTCCCTAGGCGCAT	420
Db	409	CATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCGTAGTCCCTAGGCGCAT	468
QY	421	CAATGACCCAGCTTTGGCTCGATCGAGAGCTGCGCCACCGCTATCGGGTGCATGCTG	480
Db	469	CAATGACCCAGCTTTGGCTCGATCGAGAGCTGCGCCACCGCTATCGGGTGCATGCTG	527
QY	481	CCGAGACGGTGTATGGACAGTGTGTTGCGTACCTCGATAGTGGCAGCATAAGTGAAGTCA	540
Db	528	CCGAGACGGTGTATGGACAGTGTGTTGCGTACCTCGATAGTGGCAGCATAAGTGAAGTCA	587
QY	541	CAAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAATTT	600
Db	588	CAAAAGCAAGAGGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAATTT	647
QY	601	ATATGTGGCAAAATTTATTTTGGTACTTTATATATAGGGATATGCGGCTTTTGGCACTA	660
Db	648	ATATGTGGCAAAATTTATTTTGGTACTTTATATATAGGGATATGCGGCTTTTGGCACTA	707
QY	661	TGATATTAATCGTATTATATAACAATATCATATCTTTGACTAATTTATAACAATAATAT	720
Db	708	CGGATATTAATCGTATTATATAACAATATCATATCTTTGACTAATTTATAACAATAATAT	767
QY	721	TACAAATATGATTTGGTAAACGTTGAGGTGGCAAAATGTATAAGAGCCGCTTAATAATTA	780
Db	768	TACAAATATGATTTGGTAAACGTTGAGGTGGCAAAATGTATAAGAGCCGCTTAATAATTA	827
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QY	841	ATAAATCTGTATGTCGAGGAACTTTTCTTAAACTAAATATTTAAAGCAGCTATTTT	900
Db	888	ATAAATCTGTATGTCGAGGAACTTTTCTTAAACTAAATATTTAAAGCAGCTATTTT	947
QY	901	AATATTTTTCGTCGCAAGTTTCTTGCACTATCTATCTATGCCCATTTTACTTTTATCG	960
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Db	1008	TTCTAGCCTTCTAGGTACGCTTTTGAACATAAAAAATCATAAAAATGAAAGTAAAAAT	1067
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QY	1078	ATCATTTCTGATTTTAAATATCAATACTTATCTCATGATGGAACGCTATCGTGAATCGT	1137

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Db	1245	ATTAAAGAACCCCTTATTTGATGCAAAAGTCAATAAA- - -TATTTAATATCATNCTTTAT	1304
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Db	1545	TTGCAGAAATTAATGAGGCAATAAAGTCTATGTTGGAAGTGTGTTGCTTTC	1595

RESULT 3

AX665979

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

AX665979

Sequence 2 from Patent WO02059333.

AX665979

AX665979.1

GI:29290848

Solanum tuberosum (potato)

Solanum tuberosum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

1 Dai, Z., Shi, L. and Hooker, B.S.

Gene promoters isolated from potato and use thereof

Patent: WO 02059333-A 2 01-AUG-2002;

Dai, Ziyu (US) ; Shi, Lifang (US) ; Hooker, Brian, S. (US)

Location/Qualifiers

1. .1598

/organism="Solanum tuberosum"

/mol_type="unassigned DNA"

/db_xref="taxon:4113"

ORIGIN

Query Match 86.3%; Score 1334.4; DB 6; Length 1598;

Best Local Similarity 93.8%; Pred. No. 1.6e-259;

Matches 1456; Conservative 0; Mismatches 87; Indels 10; Gaps 6;

1 ATCTTTGTTTGAATAAATTTGAAAGAACGTTAGGACCAATGACCTTGGTGCACAAAT

60

49 ATCTTTGTTTGAATAAATTTGAAAGAACGTTAGGACCAATGACCTTGGTGCACAAAT

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61 ATTGTGTCCTCCAAATGTTGTAAGAAATGTTTACATCCTCCGGGTAATTTAAGCTGAC

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109 ATTGTGTCCTCCAAATGTTGTAAGAAATGTTTACATCCTCCGGGTAATTTAAGTTGAC

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121 TAGGACATTCACCAATTTATTTTCCGTCGATGAAATGCGTGGCAATTTCCCTCCACTTG

180

169 CAGGCAATTCACCAATTTATTTTCCGTCGATGAAATGCGTGGCAATTTCCCTCCACTTG

228

181 GATTAGTCGGGGGAAAGTCAATCGGTATTTAAATCCATCAACTTAAAGAAATGTCACAGA

240

229 GATTAGTCGGGGGAAAGTCAATCGGTATTTAAATCCATCAACTTAAAGAAATGTCACAGA

288

241 AATCTAAGTTGTTGAACTCGTCCGAGGCTACTCGGCTAGGCTGTTTGGCGGTTTACCC

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289 AATCTAAGTTGTTGAACTCGTCCGAGGCTACTCGGCTAGGCTGTTTGGTGGTTGCCCC

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301 ACCCGTGTACGTCGAGGACACCAATCAACAGTCAATGACGAACTCTACACGAC

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349 ACCCGTGTACGTCGAGGACACCAATCAACAGTCAATGACGAACTCTACACGAC

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RESULT 4
 SC81OLP 2659 bp DNA linear PLN 27-OCT-1995
 LOCUS S.commersonii (posML81) gene for osmotin-like protein.
 DEFINITION X72927
 ACCESSION X72927.1 GI:296773
 VERSION osmotin-like protein.
 KEYWORDS Solanum commersonii (Commerson's wild potato)
 SOURCE Solanum commersonii
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE 1
 AUTHORS Zhu, B., Chen, T. H. and Li, P. H.
 TITLE Activation of two osmotin-like protein genes by abiotic stimuli and fungal pathogen in transgenic potato plants
 JOURNAL Plant Physiology. 108 (3), 929-937 (1995)
 MEDLINE 95357444
 PUBMED 7630973
 REFERENCE 2 (bases 1 to 2659)
 AUTHORS Zhu, B.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAR-1993) B. Zhu, Oregon State University, Dept of Horticulture, AG. & Life Science 4037, Corvallis, OR 97331, USA
 COMMENT Related sequences: M29279 & M21346.
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TATA signal
 mRNA
 CDS

ORIGIN
 Query Match 46.2%; Score 715; DB 8; Length 2659;
 Best Local Similarity 74.7%; Pred. No. 2.4e-134;
 Matches 1170; Conservative 0; Mismatches 180; Indels 217; Gaps 13;
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 Db 308 TGCTTTC 302

RESULT 5

SC130LP/c
 LOCUS
 DEFINITION S:commersonii (posML13) gene for osmotin-like protein.
 ACCESSION X72928
 VERSION X72928.1 GI:296771
 KEYWORDS osmotin-like protein.
 SOURCE Solanum commersonii (Commerson's wild potato)
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.
 REFERENCE 1
 AUTHORS Zhu,B., Chen,T.H. and Li,P.H.
 TITLE Activation of two osmotin-like protein genes by abiotic stimuli and fungal pathogen in transgenic potato plants
 JOURNAL Plant Physiol. 108 (3), 929-937 (1995)
 MEDLINE 95357444
 PUBMED 7630973
 REFERENCE 2 (bases 1 to 2638)
 AUTHORS Zhu,B.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAR-1993) B. Zhu, Oregon State University, Dept of Horticulture, AG. & Life Science 4017, Corvallis, OR 97331, USA
 COMMENT Related sequences: M29279 & M21346.
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 mRNA 1362..2325
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 CDS /codon_start=1

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ORIGIN

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Best Local Similarity 77.0%; Pred. No. 9.6e-104;
Matches 735; Conservative 0; Mismatches 194; Indels 25; Gaps 3;

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QY 121 TAGGACATTACCAATTTATATTTCCCGTGCATTGAATTTGGTGGCATTTCCCTCCACTTG 180
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DB 1800 GATTAGTGGGGCGAAATGTCATCGGTATATTAATCCATCAATTAAGAAATGTCGAGA 1741
QY 241 AATCTAGTTGTTCACTGTTCCAGCGGTACTCGGTAGGTGTTTGGGGTTTACCCC 300
DB 1740 AATCTAGTTGTTCACTGTTCCAGCGGTACTCGGTAGGTGTTTGGGGTTTACCCC 1681
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DB 1680 ACCCGGTGCTGCTGAGGACACCAACCAATCACCAGTTCATGACGACCTCTACCAAGCAC 1621
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QY 421 CAATGACCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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QY 823 TGGTGATAACTTGGACATATAAACTCTGTATCGTGACGGAACCTTTCTTAAAACTAAATA 882

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RESULT 6
AF093743/c
LOCUS AF093743
DEFINITION Lycopersicon esculentum pathogenesis-related protein osmotin precursor (NP24) gene, complete cds.
ACCESSION AF093743
VERSION AF093743.1 GI:3747059
KEYWORDS
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 1304)
AUTHORS Jia, Y. and Martin, G.B.
TITLE Rapid transcript accumulation of pathogenesis-related genes during an incompatible interaction in bacterial speck disease-resistant tomato plants
JOURNAL Plant Mol. Biol. 40 (3), 455-465 (1999)
MEDLINE 99364540
PUBMED 10437829
REFERENCE 2 (bases 1 to 1304)
AUTHORS Martin, G.B. and Jia, Y.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-1998) Boyce Thompson Institute, Tower Road, Ithaca, NY 14853-1801, USA
FEATURES
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Query Match 35.6%; Score 550.4; DB 8; Length 1304;
Best Local Similarity 78.7%; Pred. No. 4.5e-101;
Matches 711; Conservative 0; Mismatches 181; Indels 12; Gaps 4;

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DB 852 ATTGTTGCTCTCAAAATGTGTGAACAAGATTGTTACATCTCTCCGGGTACTTTTAAGCTGAC 793
QY 121 TAGGACATTACCAATTTATATTTCCCGTGCATTAAGTTGGTGGCATTTCCCTCCACTTG 180
DB 792 GAGGACATTACCAATTTATATTTGGCCGTGCAATGAATTTGGTGGCATTTTCTCTCCACTAG 733

AUTHORS		Zhao, B.	
TITLE		Direct Submission	
JOURNAL		Submitted (02-JUL-1992) B. Zhao, Dept of Horticulture, AG & Life Science 4017, Oregon State University, Corvallis OR 97331, USA	
FEATURES		Location/Qualifiers	
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QY	361	CATCAAGTTTACATCCAGTAGGACCCCATATATCGTGCATCTGTTAGTGCCTTAGGCGCAT	420
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QY	421	CAATGACCCAGTTTGGCTCGATTCGAGAGAGTTCGGCCACCGCTATCGGGGTGATGTCCTG	480
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NTOSPR/c
 LOCUS NTOSPR 2033 bp DNA linear PLN 01-FEB-1996
 DEFINITION N.tabacum osmotin gene.
 ACCESSION X95308
 VERSION X95308.1 GI:1167853
 KEYWORDS osmotin; PR protein.
 SOURCE Nicotiana tabacum (common tobacco)
 ORGANISM Nicotiana tabacum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Nicotiana.
 REFERENCE 1
 AUTHORS Barnard, W.M. and Neale, A.D.
 TITLE Comparison of the 5 regulatory regions of homeologous osmotin genes
 from Nicotiana tabacum
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2033)
 AUTHORS Neale, A.D.
 TITLE Direct Submission
 JOURNAL Submitted (24-JAN-1996) A.D. Neale, Monash University, Genetics and
 Developmental Biology, Wellington Rd, Clayton, Victoria, 3168,
 Australia
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 Db 921 ATTTGGTGAATGCTGACCTATAAGCTCTGTAACTGAC 882
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 AR037158/c 3033 bp DNA linear PAT 29-SEP-1999
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 DEFINITION Sequence 1 from patent US 5801028.
 ACCESSION AR037158
 VERSION AR037158.1 GI:5955014
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 3033)
 AUTHORS Bressan, R. and Hasegawa, P.M.
 TITLE Osmotin gene promoter and use thereof
 JOURNAL Patent: US 5801028-A 1 01-SEP-1998;
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QY 2439 GGTTAAGTCGGGCGGAAGTCTCGGTATTAATTCATCACTAAAGAAATGCCAGA 2380
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QY 241 AATCTAAGTTGTTGAACCTGTCGAGGCGTACTCGGTAGGCTGTTGGCGGTTTACCCC 300
Db |||||
QY 2379 AATCTAAGTTGTTGAACCTGTCGAGGCGTACTCGGTAGGCTGTTGGCGGTTTACCCC 2320
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RESULT 10
S40046/c
LOCUS
DEFINITION
S40046
ACCESSION
VERSION

S40046
abscisic acid-activated
Genomic, 3033 nt].

linear
Nicotiana tabacum L. tobacco, leaf,

3033 bp
DNA

PLN 17-APR-2000

GI:251138

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
MEDLINE
PUBMED
REMARK

FEATURES
source

gene
CDS

ORIGIN

Query Match 32.3%; Score 500; DB 8; Length 3033;
Best Local Similarity 71.1%; Pred. No. 6.9e-91;
Matches 749; Conservative 0; Mismatches 265; Indels 40; Gaps 5;

QY 1 ATCTTTGTTTGAATAATTTGGAAGAACGTTAGGACCAATGCTTGGGTGCAACAAT 60
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QY 2619 ATCTTTGTTTGAATAATTTTGAATAATTTTGAATAATTTTGAATAATTTTGAATAAT 2560
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QY 2499 GGGGACATTCGCGTTTATTTAGCGGTACAAATGTTGATGTCATGTCATGTCATGTCATG 2440
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Db |||||

Nicotiana tabacum (common tobacco)
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 3033)
Nelson, D.E., Raghothama, K.G., Singh, N.K., Haese, P.M. and
Bressan, R.A.
Analysis of structure and transcriptional activation of an osmotin
gene
Plant Mol. Biol. 19 (4), 577-588 (1992)
92329718
1385735
GenBank staff at the National Library of Medicine created this
entry [NCBI gi303310842] from the original journal article.
This sequence comes from Fig. 1A.
Location/Qualifiers
1..3033
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2034..2774
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/note="basic PR-like protein; This sequence comes from
Fig. 1A; conceptual translation presented here differs
from translation in publication; mismatch(181[R->G])"
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DEFINITION N.tabacum ap24 gene.
ACCESSION X65701
VERSION X65701.1 GI:19782
KEYWORDS osmotin.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
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REFERENCE
AUTHORS Melchers,L.S., Sela-Buuriage,M.B., Vloemans,S.A., Woloshuk,C.P.,
Van Roekel,J.S., Pen,J., van den Elzen,P.J. and Cornelissen,B.J.
TITLE Extracellular targeting of the vacuolar tobacco proteins AP24,
chitinase and beta-1,3-glucanase in transgenic plants
JOURNAL Plant Mol. Biol. 21 (4), 583-593 (1993)
MEDLINE 93192519
PUBMED 8448358
REFERENCE
AUTHORS Melchers,L.S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-1992) L.S. Melchers, Mogen International NV,
Einsteinweg 97, 2333 CB Leiden, THE NETHERLANDS
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Db 964 ATTGTTGCTTCCCAATGTGTGTACAGGATTTTACATCTCCCGGTACTTTAAGCTGAC 905
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LOCUS S.commersonii (pA81) mRNA for osmotin-like protein.
DEFINITION X72926
ACCESSION X72926.1 GI:296775
VERSION osmotin-like protein.
KEYWORDS Solanum commersonii (Commerson's wild potato)
SOURCE Solanum commersonii
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 977)
AUTHORS Zhu, B., Chen, T.H. and Li, P.H.
TITLE Expression of three osmotin-like protein genes in response to
osmotic stress and fungal infection in potato
JOURNAL Plant Mol. Biol. 28 (1), 17-26 (1995)
MEDLINE 9306785
PUBMED 7787181
REFERENCE 2 (bases 1 to 977)
AUTHORS Zhu, B.
TITLE Direct Submission
JOURNAL Submitted (29-MAR-1993) B. Zhu, Oregon State University, Dept of
Horticulture, AG. & Life Science 4017, Corvallis, OR 97331, USA
COMMENT Related sequences: M29279 & M21346.
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LOCUS Lycopersicon esculentum PR-5x (PR-5) mRNA, complete cds.
DEFINITION AY093595
ACCESSION AY093595
VERSION AY093595.1 GI:20750096
KEYWORDS Lycopersicon esculentum (tomato)
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 917)
AUTHORS Rep.M., Dekker, H.L., Vossen, J.H., De Boer, A.D., Houterman, P.M.,
Speijer, D., Back, J.W., De Koster, C.G. and Cornelissen, B.J.C.
TITLE Mass Spectrometric Identification of Isoforms of PR Proteins in
Xylem Sap of Fungus-Infected Tomato
JOURNAL Plant Physiol. 130 (2), 904-917 (2002)
MEDLINE 22264016
PUBMED 12376655

REFERENCE 2 (bases 1 to 917)
 AUTHORS Rep.M., Dekker H., Vossen, J.H., de Boer, A., Houterman, P.,
 Speijer, D., Back, J.-W. and Cornelissen, B.J.C.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAR-2002) Plant Pathology, University of Amsterdam,
 Kruislaan 318, Amsterdam 1098SM, Netherlands

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 DB 5 TTTTG 1

RESULT 14
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 LOCUS AF473702 729 bp DNA linear PLN 25-FEB-2002
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 ACCESSION AF473702
 VERSION AF473702.1 GI:18874518
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 Solanum nigrum (black nightshade)
 Solanum nigrum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.
 REFERENCE 1 (bases 1 to 729)
 AUTHORS Jami, S.K. and Kirti, P.B.
 TITLE PCR-based cloning of an osmotin-like protein gene from Solanum
 nigrum
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 729)
 AUTHORS Jami, S.K. and Kirti, P.B.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2002) Department of Plant Sciences, University of
 Hyderabad, Gachibowli, Hyderabad, A.P 500046, India

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QY 1 ATCTTTGTTGAAATAATTGGAAGAAGACCTAGGACACATGACCTGGTGGTGCACAAAT 60
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